STIC Search Report
Biotech-Chem Library

USPTO — Scientific & Technical Information Center

TO: Celine Qian
Location: REM/2A64/2C70
Art Unit: 1636
Tuesday, July 05, 2005

Case Serial Number: 09/921143

From: Edward Hart
Location: Biotech-Chem Library
REM-1A55
Phone: 571-272-2512

edward.hart@uspto.gov

Search Notes

Examiner Qian,

Here are the results of the search you requested.

Please feel free to contact me if you have any questions.

Edward Hart

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STIC SEARCH RESULTS FEEDBACK FORM

Biotech-Chem Library

Questions about the scope or the results of the search? Contact **the searcher or contact**:

Mary Hale, Information Branch Supervisor
Remsen Bldg. 01 D86
571-272-2507

Voluntary Results Feedback Form

➤ *I am an examiner in Workgroup:* ☐ *Example: 1610*

➤ *Relevant prior art **found**, search results used as follows:*

- ☐ 102 rejection
- ☐ 103 rejection
- ☐ Cited as being of interest.
- ☐ Helped examiner better understand the invention.
- ☐ Helped examiner better understand the state of the art in their technology.

   Types of relevant prior art found:
   - ☐ Foreign Patent(s)
   - ☐ Non-Patent Literature
      (journal articles, conference proceedings, new product announcements etc.)

➤ *Relevant prior art **not found**:*

- ☐ Results verified the lack of relevant prior art (helped determine patentability).
- ☐ Results were not useful in determining patentability or understanding the invention.

Comments:

sira
Search and Information

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SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: __Celine Qian__   Examiner # : __78710__ Date: __6/28/05__

Art Unit: __1656__   Phone Number: 30__2-0777__ , Serial Number: __09/921143__

Mail Box and Bldg/Room Location: __2A64__   Results Format Preferred (circle): (PAPER) DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.
****

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of invention: __Vascular Endothelial Growth Factor - 2__

Inventors (please provide full names): __Coleman, Timothy__

Earliest Priority Filing Date: __8/3/2000__

For Sequence Searches Only Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

Please search SEQ ID NO:36 . (both commercial and interference). Thank you.

NA 5283

Mé'

* *

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 3, 2005, 01:14:22 ; Search time 21907 Seconds
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Title: US-09-921-143-36
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Searched: 4708233 seqs, 2422607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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             12: gb_sy:*
             13: gb_un:*
             14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1		2410	45.6	6074	12	CVE18316	Y18316 Cloning vec
2		2240	42.4	8349	6	AR260588	AR260588 Sequence
3	c	2233.4	42.3	2661	12	SYN8KMRCG	M17626 Synthetic p
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9	c	2088.4	39.5	3036	12	AY222815	AY222815 Cloning v
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ALIGNMENTS

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DEFINITION Cloning vector pKGlM.
ACCESSION   Y18316
VERSION   Y18316.1 GI:5830187
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SOURCE   Cloning vector pKGlM
  ORGANISM Cloning vector pKGlM
            other sequences; artificial sequences; vectors.
REFERENCE   1
  AUTHORS   Bannasch,D. and Schwab,M.
  TITLE   A versatile bait vector for rapid Gal4 dependent two-hybrid screens
  JOURNAL   Unpublished
REFERENCE   2 (bases 1 to 6074)
  AUTHORS   Bannasch,D.
  TITLE   Direct Submission
  JOURNAL   Submitted (30-OCT-1998) D. Bannasch, Institution Division of,
            Cytogenetics/H0400 Deutsches, Krebsforschungszentrum (DKFZ), Im
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promoter        complement(4410. .4459)
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ORIGIN

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Matches 2568;   Conservative   0;   Mismatches   5;   Indels 145;   Gaps 1;

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Qy   2771 ACATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCA 2830
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Qy   3011 CAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAG 3070
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Qy   3251 TTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGC 3310
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KEYWORDS     .
SOURCE       Unknown.
  ORGANISM   Unknown.
             Unclassified.
REFERENCE    1  (bases 1 to 8349)
  AUTHORS    Corbin,D.R. and Romano,C.P.
. TITLE      Methods for transforming plants to express Cry2Ab
             .delta.-endotoxins targeted to the plastids
  JOURNAL    Patent: US 6489542-A 16 03-DEC-2002;
FEATURES     Location/Qualifiers
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ORIGIN

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Best Local Similarity  93.4%;  Pred. No. 0;
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Qy    3366 GCTGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTA 3425
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Db    6571 GCTGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTA 6630

Qy    3426 TCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCCACTGGTAA 3485
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Db    6631 TCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCCACTGGTAA 6690

Qy    3486 CAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAA 3545
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Db    3694 CACAGTCCATGAATCCAGAAAAGCGGCCATTTTCCACCATGATATTCGGCAAGCAGGCAT 3753
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Qy    4366 CGCCATGGGTCACGACGAGATCCTCGCCGTCGGGCATGCGCGCCTTGAGCCTGGCGAACA 4425
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Db    3754 CGCCATGGGTCACGACGAGATCCTCGCCGTCGGGCATGCGCGCCTTGAGCCTGGCGAACA 3813

Qy    4426 GTTCGGGCTGGCGGCGAGCCCCTGATGCTCTTCGTCCAGATCATCCTGATCGACAAGACCGG 4485
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Db    3814 GTTCGGGCTGGCGGCGAGCCCCTGATGCTCTTCGTCCAGATCATCCTGATCGACAAGACCGG 3873

Qy    4486 CTTCCATCCGAGTACGTGCTCGCTCGATGCGATGTTTCGCTTGGTCGTGGTCGAATGGGCAGG 4545
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3874 CTTCCATCCGAGTACGTGCTCGCTCGATGCGATGTTTCGCTTGGTCGTGGTCGAATGGGCAGG 3933

Qy    4546 TAGCCGGATCAAGCGTATGCAGCGCGCCCATTGCATCAGCCATGATGATACTTTCTTCGG 4605
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Db    3934 TAGCCGGATCAAGCGTATGCAGCGCGCCCATTGCATCAGCCATGATGATACTTTCTTCGG 3993

Qy    4606 CAGGAGCAAGGTGAGATGACAGGAGATCCTGCCCCGGCACTTCGCCCAATAGCAGCCAGT 4665
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Db    3994 CAGGAGCAAGGTGAGATGACAGGAGATCCTGCCCCGGCACTTCGCCCAATAGCAGCCAGT 4053

Qy    4666 CCCTTCCCGCTTCAGTGACAACGTCGAGCACACGACAGCTGCGCAAGGAACGCCCGTCGTGGCCA 4725
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Db    4054 CCCTTCCCGCTTCAGTGACAACGTCGAGCACACGACAGCTGCGCAAGGAACGCCCGTCGTGGCCA 4113

Qy    4726 GCCACGATAGCCGCGCTGCCTCGTCCTGCAGTTCATTCAGGGCACCGGACAGGTCCGTCT 4785
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Db    4114 GCCACGATAGCCGCGCTGCCTCGTCCTGCAGTTCATTCAGGGCACCGGACAGGTCCGTCT 4173

Qy    4786 TGACAAAAGAAACCGGGCGCCCGCTGACAGCCGGAACAACGGCGGCGATCAGCAGCAGC 4845
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Db    4174 TGACAAAAGAAACCGGGCGCCCGCTGACAGCCGGAACAACGGCGGCGATCAGCAGCAGC 4233

Qy    4846 CGATTGTCTGTTGTGCCCAGTCATAGCCGGAATAGCCTTCCACCCAAGCGGCCGGAGAAC 4905
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Db    4234 CGATTGTCTGTTGTGCCCAGTCATAGCCGGAATAGCCTTCCACCCAAGCGGCCGGAGAAC 4293

Qy    4906 CTGCGTGCAATCCATCTGTTCAATCATGCGAAACGATCCTCATCCTGTCTCCTTGATCAG 4965
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Db    4294 CTGCGTGCAATCCATCTGTTCAATCATGCGAAACGATCCTCATCCTGTCTCTTGATCAG 4353

Qy    4966 ATCTTGATCCCCTGCGCCATCAGATCCCTTGGCGGCCAAGAAAGCCATCCAGTTTACTTTGC 5025
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Qy    5026 AGGGCTTCCCAACCTTACCAGAGGGCGCCCCAGCTGGCAATTCCGGTTCGCTTGCTGTCC 5085
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Db    4414 AGGGCTTCCCAACCTTACCAGAGGGCGCCCCAGCTGGCAATTCCGGTTCGCTTGCTGTCC 4473

Qy    5086 ATAAAACCGCCCAGTCTAGCTATCGCCATGTAAGGCCATGGCCAGTGAGCGCTTGCTTTCT 5145
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Qy    5146 TTGCGCTTGGCTTTCTCGCGGGTTTCCCTTGTCCAGATAGCCCAGTAGCTGACATTCATCCGGGGTCAGC 5205
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4534 TTGCGCTTGGCTTTCTCGCGGGTTTCCCTTGTCCAGATAGCCCAGTAGCTGACATTCATCCGGGGTCAGC 4593

Qy    5206 ACCGTTTTCTGCGGACTGGCTTTCTACGCGGTTCCGCTTCCTTTAGCAGCCCTGCGCCCTG 5265
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Db    4594 ACCGTTTTCTGCGGACTGGCTTTCTACGCGGTTCCGCTTCCTTTAGCAGCCCTGCGCCCTG 4653

Qy    5266 AGTGCTTGCGGCAGCGTG 5283
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Db    4654 AGTGCTTGCGGCAGCGTG 4671
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RESULT 2
AR260588
LOCUS       AR260588      8349 bp   DNA      linear   PAT 20-DEC-2002
DEFINITION  Sequence 16 from patent US 6489542.
ACCESSION   AR260588
VERSION     AR260588.1  GI:27311143
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Db   6691  CAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAA  6750

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           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   6751  CTACGGCTACACTAGAAGAACAGTATTTGGTATCGCGCTCTGCTGAAGCCAGTTACCTT   6810

Qy   3606  CGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTT  3665
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   6811  CGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTT  6870

Qy   3666  TTTTGTTTGCAAGCAGCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGAT  3725
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Db   6871  TTTTGTTTGCAAGCAGCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGAT  6930

Qy   3726  CTTTTCTACGGGGTCTGACGCTCAGTGGAACGAAAACTCACGTTAAGGGATTTTGGTCAT  3785
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Qy   3786  GAGATTATCGTCGACCAAAGGGCCATCGTGCCTCCCCACTCGTGCCAGTTCGGGGGGCATG  3845
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Db   6991  GAGATTATCAAAAAGGATCTTCACCTAGATCCTT-----------------------    7024

Qy   3846  GATGCGCGGATAGCCGCTGCTGGTTTCCTGATGCCGACGGATTTGCACTGCCGGTAGAA   3905
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Qy   3906  CTCCGCGAGTCGTCCAGCCTGCAGCAGCTGAACCAACTCGGCGAGGGGGATCGAGCCC   3965
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Db   7025  CTCCGCGAGTCGTCCAGCCTGCAGCAGCTGAACCAACTCGGCGAGGGGGATCGAGCCC--TT  7026

Qy   3966  GGGGTGGCGGAAGAACTCCAGCATGAGATCCCGCGCTGGAGGATCATCCAGCCGCCGTC  4025
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Db   7027  GGGGTGGCGGAAGAACTCCAGCATGAGATCCCGCGCTGGAGGATCATCCAGCCGCCGTC  7086

Qy   4026  CCGGAAAACGATTCCGAAGCCCAACCTTTCATAGAAGGCGGCGGTGGAATCGAAATCTCG  4085
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Db   7087  CCGGAAAACGATTCCGAAGCCCAACCTTTCATAGAAGGCGGCGGTGGAATCGAAATCTCG  7146

Qy   4086  TGATGGCAGGTTGGGCGTCGCTTGGTCGGTCATTTCGAACCCCAGAGTCCCGCTCAGAAG  4145
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Db   7147  TGATGGCAGGTTGGGCGTCGCTTGGTCGGTCATTTCGAACCCCAGAGTCCCGCTCAGAAG  7206

Qy   4146  AACTCGTCAAGAAGGCGATAGAAGGCGATGCGCTGCGAATCGGGAGCGGCGATACCGTAA  4205
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Db   7207  AACTCGTCAAGAAGGCGATAGAAGGCGATGCGCTGCGAATCGGGAGCGGCGATACCGTAA  7266

Qy   4206  AGCACGAGGAAGCGGTCAGCCCATTCGCCGCCAAGCTCTTCAGCAATATCACGGGTAGCC  4265
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Db   7267  AGCACGAGGAAGCGGTCAGCCCATTCGCCGCCAAGCTCTTCAGCAATATCACGGGTAGCC  7326

Qy   4266  AACGCTATGTCCTGATAGCGGTCCGCCACACCCAGCCGGCTTCATCCGATGAATCCAGAA  4325
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Db   7327  AACGCTATGTCCTGATAGCGGTCCGCCACACCCAGCCGGCTTCATCCGATGAATCCAGAA  7386

Qy   4326  AAGCGGCCATTTTCCACCATGATATTCGGCAAGCAGGCATCGCCATGGGTCACGACGAGA  4385
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Db   7387  AAGCGGCCATTTTCCACCATGATATTCGGCAAGCAGGCATCGCCATGGGTCACGACGAGA  7446

Qy   4386  TCCTCGCCGTCGGGCATGCGCGCCTTGAGCCTGGCGAACAGTTCGGCTGGCGCGAGCCCC  4445
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Db   7447  TCCTCGCCGTCGGGCATGCGCGCCTTGAGCCTGGCGAACAGTTCGGCTGGCGCGAGCCCC  7506

Qy   4446  TGATGCTCTTCGTCCAGATCATCCTGATCGACAAGACCGGCTTCCATCCGAGTACGTGCT  4505
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Db   7507  TGATGCTCTTCGTCCAGATCATCCTGATCGACAAGACCGGCTTCCATCCGAGTACGTGCT  7566

Qy   4506  CGCTCGATGCGATGTTTCGCTTGGTGGTCGAATGGGCAGCAGGTAGCCGGATCAAGCGTATGC  4565
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Db   7567  CGTTCGATGCGATGTTTCGCTTGGTGGTCGAATGGGCAGCAGGTAGCCGGATCAAGCGTATGC  7626

Qy   4566  AGCCGCCGCATTGCATCAGCCATGATGGATACTTTCTCGGCAGGAGCAAGGTGAGATGAC  4625
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Db   7627  AGCCGCCGCATTGCATCAGCCATGATGGATACTTTCTCGGCAGGAGCAAGGTGAGATGAC  7686
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Qy   4626  AGGAGATCCTGCCCCGGCACTTCGCCCAATAGCAGCCAGTCCCTTCCCGCTTCAGTGACA  4685
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Db   7687  AGGAGATCCTGCCCCGGCACTTCGCCCAATAGCAGCCAGTCCCTTCCCGCTTCAGTGACA  7746

Qy   4686  ACGTCGAGCACAGCTGCGCAAGGAACGGCCCGTGCGGCCAGCCACGATAGCCGCGCTGCC  4745
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Qy   4746  TCGTCCTGCAGTTCATTCAGGGCACCGGACAGGTCGGTCTTGACAAAAAGAACCGGCGC  4805
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Qy   4806  CCCTGGCCTGACAGCCGGAACACGGCGGCATCAGAGCAGCCGATTGTCTGTTGTGCCCAG  4865
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Qy   4866  TCATAGCCGAATAGCCTCTCCACCCAAGCGGCCGGAGAACCTGCGTGCAATCCATCTTGT  4925
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Db   7927  TCATAGCCGAATAGCCTCTCCACCCAAGCGGCCGGAGAACCTGCGTGCAATCCATCTTGT  7986

Qy   4926  TCAATCATGCGAAACGATCCTCATCCTGTCTCTTGATCAGATCTTGATCCCCTGCGCCAT  4985
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Db   7987  TCAATCATGCGAAACGATCCTCATCCTGTCTCTTGATCAGATCTTGATCCCCTGCGCCAT  8046

Qy   4986  CAGATCCTTGGCGGCGAAGAAGCCATCCAGTTTACTTTGCAGGGCTTCCCAACCTTACCA  5045
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Db   8047  CAGATCCTTGGCGGCGAAGAAGCCATCCAGTTTACTTTGCAGGGCTTCCCAACCTTACCA  8106

Qy   5046  GAGGGCGCCCCAGCTGGCAATTCCGGTTCGCTTGCTGTCCATAAAACCGCCAGTCTAGC  5105
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Qy   5106  TATCGGCATGTAAGCCCACTGCAAGCTACCTGCTTTCTCTTTGCGCTTGCGTTTTCCCTT  5165
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Db   8167  TATCGGCATGTAAGCCCACTGCAAGCTACCTGCTTTCTCTTTGCGCTTGCGTTTTCCCTT  8226

Qy   5166  GTCCAGATAGCCCAGTAGCTGACATTCATCCGGGGTCAGCACCGTTTCTGCGGACTGGCT  5225
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Db   8227  GTCCAGATAGCCCAGTAGCTGACATTCATCCGGGGTCAGCACCGTTTCTGCGGACTGGCT  8286

Qy   5226  TTCTACGTGTTCCGCTTCCTTTAGCAGCCCTTGCGCCCTGAGTGCTTGCGGCAGCGTG   5283
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Db   8287  TTCTACGTGTTCCGCTTCCTTTAGCAGCCCTTGCGCCCTGAGTGCTTGCGGCAGCGTG   8344
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RESULT 3

SYN8KMRCG/c

LOCUS   SYN8KMRCG   2661 bp   DNA   linear   SYN 27-APR-1993
DEFINITION   Synthetic plasmid pK18 (pBRNeo/pUC18) kanamycin resistance gene,
             complete cds.
ACCESSION   M17626
VERSION   M17626.1 GI:207845
KEYWORDS   complete genome; kanamycin resistance.
SOURCE   unidentified cloning vector
  ORGANISM   unidentified cloning vector
             other sequences; artificial sequences; vectors.
REFERENCE   1 (bases 1 to 2661)
  AUTHORS   Pridmore,R.D.
  TITLE   New and versatile cloning vectors with kanamycin-resistance marker
  JOURNAL   Gene 56 (2-3), 309-312 (1987)
  MEDLINE   88056335
  PUBMED   3315864
COMMENT   Original source text: Plasmid pBRNeo and pUC18 DNA.
FEATURES   Location/Qualifiers
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                     /mol_type="genomic DNA"
                     /db_xref="taxon:45196"
     CDS   365..1159
                     /note="kanamycin"
                     /codon_start=1
                     /transl_table=11

us-09-921-143-36.rge

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                LSSHLAPAEKVSIMADAMRLRHTLDPATCPFDHQAKHRIERARTRMEAGLVDQDDLDE
                EHQGLAPAELFARLKARMPDGEDLVVTHGDACLPNIMVENGRFSGFIDCGRLGVADRY
                QDIALATRDIAEELGGEWADRFLVLYGIAAPDSQRIAFYRLLDEFF"
ORIGIN

Query Match     42.3%;   Score 2233.4;   DB 12;   Length 2661;
Best Local Similarity  93.4%;   Pred. No. 0;
Matches 2403;   Conservative  0;   Mismatches  26;   Indels  144;   Gaps  1;

Qy  2711 CGTAATCATGGTCATAGCTGTTTCCTGTGTGAAATTGTATCCGCTCACAATTCCACACA 2770
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Db  2443 CGTAATCATGGTCATAGCTGTTTCCTGTGTGAAATTGTATCCGCTCACAATTCCACACA 2384

Qy  3611 AAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACACCGCTGGTAGCGTGGTTTTTTG 3670
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Qy  2771 ACATACGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCA 2830
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Db  2383 ACATACGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCA 2324

Qy  3671 TTTGCAAGCAGCAGATTACGGCGAGAAAAAAGGATCTCAAGAAGATCTTGATCTTT 3730
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Db  1483 TTTGCAAGCAGCAGATTACGGCGAGAAAAAAGGATCTCAAGAAGATCTTGATCTTT 1424

Qy  2831 CATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTGTGCCAGCTGC 2890
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Db  2323 CATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTGTGCCAGCTGC 2264

Qy  3731 CTACGGGGTCTGACGCTCAGTGGAACGAAAACTCACGTTAAGGGATTTTGGTCATGAGAT 3790
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Qy  2891 ATTAAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTT 2950
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Qy  2951 CCTCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACT 3010
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Db  2203 CCTCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACT 2144

Qy  3851 GCGGATAGCCGCGTTGCTGGCGTTTCTGGATGCCGACGGATTTGCACTGCCGGTAGAACTCCG 3910
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Db  1334 --------------------------------------- 1335

Qy  3011 CAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAG 3070
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Db  2143 CAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAG 2084

Qy  3911 CGAGGTCGTCCAGCCTCAGGCAGCAGCTGAACCAACTCGCGAGGGGATCGAGCCGCGGGGT 3970
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Qy  3071 CAAAAGGCCAGCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATA 3130
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Qy  3971 GGGCGAAGAACTCCAGCATGAGATCCCGCGCTGGAGGATCATCCAGCCGCGTCCCGGA 4030
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Db  1327 GGGCGAAGAACTCCAGCATGAGATCCCGCGCTGGAGGATCATCCAGCCGCGTCCCGGA 1268

Qy  3131 GGCTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACC 3190
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Db  2023 GGCTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACC 1964

Qy  4031 AAACGATTCCGAAGCCCAACCTTTCATAGAAGGCGGGGTGGAATCGAAATCTCGTGATG 4090
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Qy  3191 CGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTG 3250
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Qy  4091 GCAGGTTGGGCGTCGGTTGGTCGGTCATTTGAACCCCAGCTCCCGCTCAGAAGAACTC 4150
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Qy  3251 TTCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGC 3310
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Db  1843 TTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGG 1784

Qy  4211 GAGGAAGCGGTCAGCCCATTCGCCGCCAAGCTCTTCAGCAATATCACGGGTAGCCAACGC 4270
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Qy  3371 GCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTC 3430
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Db  1783 GCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTC 1724

Qy  4271 TATGTCCTGATAGCGGTCCGCCACACCCAGCCGGCCACAGTCGATGAATCCAGAAAAGCG 4330
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1027 TATGTCCTGATAGCGGTCCGCCACACCCAGCCGGCCACAGTCGATGAATCCAGAAAAGCG 968

Qy  3431 TTGAGTCCAACCCGGTAAGACACGACTTATCGCCAGCAGCCACTGGTAACAGGA 3490
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1723 TTGAGTCCAACCCGGTAAGACACGACTTATCGCCAGCAGCCACTGGTAACAGGA 1664

Qy  4331 GCCATTTTCCACCATGATATTCGGCAAGCAGGCATCGGCGGTGCAACGCTCAGCGC 4390
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Db  967  GCCATTTTCCACCATGATATTCGGCAAGCAGGCATCGGCGGTGCAACGCTCAGCGC 908

Qy  3491 TTACGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACG 3550
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1663 TTACGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACG 1604

Qy  4391 GCCGTGGAGTCGCGCGCCCTGAGCCTGGGAACAGTTCGGCTGGCGGCCGAGCCCCTGATG 4450
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  907  GCCGTGGAGTCGCGCGCCCTGAGCCTGGGAACAGTTCGGCTGGCGGCCGAGCCCCTGATG 848

Qy  3551 GCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAA 3610
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1603 GCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAA 1544

Qy  4451 CTCTTCGTTCGTGCCAGATCATCCTCGATCTCCTGATCGACAAGACCGGCTTCATCCGGCTCGTC 4510
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Db  847  CTCTTCGTTCGTGCCAGATCATCCTCGATCTCCTGATCGACAAGACCGGCTTCATCCGGCTCGTC 788

Qy  4691 GAGCAGAGCTGCGCAAGGAACGCCCGTCGTGCGCCACGATAGCCGCGCTGCCTCGTC 4750

Qy  4511 GATGCCGATGTTTCGCTTGGTGTGTGTTGGCCAGTTCCGGCAGGTAGCCAAGCGTATGCAGCCG 4570
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Db  787  GATGCCGATGTTTCGCTTGGTGTGTGTTGGCCAGTTCCGGCAGGTAGCCAAGCGTATGCAGCCG 728

Qy  4571 CCGCATTGCATCAGCCATGATGGATACTTTCTCGGCAGGAGCAAGGTGAGATGACAGGAG 4630
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  727  CCGCATTGCATCAGCCATGATGGATACTTTCTCGGCAGGAGCAAGGTGAGATGACAGGAG 668

Qy  4631 ATCCTCGCCCCGGCACTTCGCCCAATAGCAGCCAGTCCCTTCCCGCTTCAGTGACAACGTC 4690
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  667  ATCCTCGCCCCGGCACTTCGCCCAATAGCAGCCAGTCCCTTCCCGCTTCAGTGACAACGTC 608
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ORIGIN

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Query Match                    42.0%;    Score 2218.4;   DB 12;  Length 2999;
Best Local Similarity          93.4%;    Pred. No. 0;
Matches 2388;  Conservative  26;  Indels 144;  Gaps  1;
                               0;  Mismatches

EEVADLSHRENDIKNAINLMFWGI"
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Qy   2726 AGCTGTTCCTGTGTGAAATTGTTATCCGCTCACAATTCCACACAACATACGAGCCGGAA 2785
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Db   2999 AGCTGTTCCTGTGTGAAATTGTTATCCGCTCACAATTCCACACAACATACGAGCCGGAA 2940

Qy   2786 GCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACATTAATTGCGTTGC 2845
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Qy   2846 GCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCATTAATGAATCGGCC 2905
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Db   2879 GCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCATTAATGAATCGGCC 2820

Qy   2906 AACGGCGCGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTTCCTCGCTCACTGACT 2965
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Db   2819 AACGGCGCGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTTCCTCGCTCACTGACT 2760

Qy   2966 CGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCAAAGGCGGTAATAC 3025
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Db   2759 CGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCAAAGGCGGTAATAC 2700

Qy   3026 GGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCAAAAGGCCAGCAAA 3085
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Db   2699 GGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCAAAAGGCCAGCAAA 2640

Qy   3086 AGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCCTG 3145
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2639 AGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCCTG 2580

Qy   3146 ACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAA 3205
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Db   2579 ACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAA 2520

Qy   3206 GATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGC 3265
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Db   2519 GATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGC 2460

Qy   3266 TTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGTCAC 3325
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Db   2459 TTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGTCAC 2400

Qy   3326 GCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTGCACGAAC 3385
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Db   2399 GCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTGCACGAAC 2340

Qy   3386 CCCCCGTTCAGCCCGACCGCTGCGCCTTATCGGTAACTATCGTCTTGAGTCCAACCCGG 3445
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Db   2339 CCCCCGTTCAGCCCGACCGCTGCGCCTTATCGGTAACTATCGTCTTGAGTCCAACCCGG 2280

Qy   3446 TAAGACAGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGT 3505
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Db   2279 TAAGACAGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGT 2220

Qy   3506 ATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTACTACGGCTACACTAGAAGAA 3565
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Db   2219 ATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTACTACGGCTACACTAGAAGAA 2160

Qy   3566 CAGTATTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCT 3625
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Db   2159 CAGTATTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCT 2100

Qy   3626 CTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTGTTGCCAAGCAGCAGA 3685
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Db   2099 CTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTGTTGCCAAGCAGCAGA 2040

Qy   3686 TTACGGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACG 3745
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Db    607 GAGCACCAGCTGCGCAAGGAGCGACCCGTCGTGGCCAGCGATAGCCGGCGCCGCCTCGTC 548

Qy   4751 CTGCAGTTCATTCAGGGCACCGGACAGGTCGGTCTTGACAAAGAACCGGCGCCCCCTG 4810
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Db    547 TTGGAGTTCATTCAGGGCACCGGACAGGTCGGTCTTGACAAAAGAACCGGCGCCCCCTG 488

Qy   4811 CGCTGACAGCCGGAACACGGCGCGCATCAGAGCAGCCGATTGTCTGTTGTGCCCAGTCATA 4870
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    487 CGCTGACAGCCGGAACACGGCGCGCATCAGAGCAGCCGATTGTCTGTTGTGCCCAGTCATA 428

Qy   4871 GCCGAATAGCCTCTCCACCCAGGCCGGAGAACCTGCGTGCAATCCATCCATCTTGTTCAAT 4930
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    427 GCCGAATAGCCTCTCCACCCAGGCCGGAGAACCTGCGTGCAATCCATCCATCTTGTTCAAT 368

Qy   4931 CATGCGAAACGATCTTCATCCTGTCTCTTGATCAGATCTTGATCCCCTGGCCATCAGAT 4990
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    367 CATGCGAAACGATCTTCATCCTGTCTCTTGATCAGATCTTGATCCCCTGGCCATCAGAT 308

Qy   4991 CCTTGCGCGGCAAGAAAGCCATCCAGTTACTTTGCAGGGCTTCCCAACCTTACCAGAGGG 5050
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Db    307 CCTTGCGCGGCAAGAAAGCCATCCAGTTACTTTGCAGGGCTTCCCAACCTTACCAGAGGG 248

Qy   5051 CGCCCCAGCTGGCAATTCCGGTTCGCTTGCTGTCCAGTCTAGTCTAGTCTATCG 5110
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    247 CGCCCCAGCTGGCAATTCCGGTTCGCTTGCTGTCCAGTCTAGTCTAGTCTATCG 188

Qy   5111 CCATGTAAGCCCACTGCAAGCTACCCGCTTCCTCTTCTGCGCTTGGCGTTTTCCCTTGTCCA 5170
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    187 CCATGTAAGCCCACTGCAAGCTACCCGCTTCCTCTTCTGCGCTTGGCGTTTTCCCTTGTCCA 128

Qy   5171 GATAGCCCAGTAGCTGACATTCATCCGGGGTTTCTGCAGCAACCGGTTTCTGCGGCTGGCTTTCTA 5230
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Db    127 GATAGCCCAGTAGCTGACATTCATCCGGGGTTTCTGCAGCAACCGGTTTCTGCGGCTGGCTTTCTA 68

Qy   5231 CGTGTTCCGCTTCCTTTAGCAGCCCTTGCGCCCTGAGTGCTTGCGGCAGCGTG 5283
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Db     67 CGTGTTCCGCTTCCTTTAGCAGCCCTTGCGCCCTGAGTGCTTGCGGCAGCGTG 15
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RESULT 4
SYNCCDBA/c
LOCUS       SYNCCDBA           2999 bp    DNA    linear    SYN 16-MAR-2000
DEFINITION  Cloning vector pKIL118 ccdB gene, complete cds and
            kanamycin-resistance (KmR) gene fragment.
ACCESSION   L38498
VERSION     L38498.1  GI:986977
KEYWORDS    ccdB gene; cloning vector; kanamycin resistance.
SOURCE      Cloning vector pKIL118
  ORGANISM  Cloning vector pKIL118
            other sequences; artificial sequences; vectors.
REFERENCE   1  (bases 1 to 2999)
  AUTHORS   Bernard.P.
  TITLE     New ccdB positive-selection cloning vectors with kanamycin or
            chloramphenicol selectable markers
  JOURNAL   Gene 162 (1), 159-160 (1995)
  MEDLINE   96009896
   PUBMED   7557407
FEATURES             Location/Qualifiers
     source          1..2999
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                     /db_xref="taxon:118286"
     gene            1..381
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     CDS             1..381
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                     /db_xref="GI:986978"
                     /translation="MTMTNSSSVPGDPLESTCRHASLSLQFKVYTYKRESRVRLFVD
                     VQSDIIDTPGRRMVIPLASARLLSDKVSRELYPVHIGDESWRMTTDMASVPVSVIG
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Db 2039 TTACGCGCAGAAAAAGAACGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACG 1980

Qy 3746 CTCAGTGGAACGAAAACTCACGTTAAGGGATTTTGGTCATGAGATTATCGTCGACCAAAG 3805
          ||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db 1979 CTCAGTGGAACGAAAACTCACGTTAAGGGATTTTGGTCATGAGATTATCAAAAAAGGATCT 1920

Qy 3806 CGGCCATCGTGCTCCCCACTCCTGCAGTTCGGGGGCATGGATGCGGGGATAGCCGCTGC 3865
          |||||||||||| |||||
Db 1919 TCACCTAGATCCTT-- 1906

Qy 3866 TGGTTTCCTGGATGCCGACGGATTTGCACTGCCGGTAGAACTCCGCGAGTCGTGTCCAGCC 3925
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1905 -- 1906

Qy 3926 TCAGGCAGCAGCTGAACCAACTCGCGAGGGGATCGAGCCCGGGGTGGCGAAGAACTCCA 3985
                              |||||||||||||||||||||||||||||||||||||
Db 1905 --------------------TTGGGGTGGGCGAAGAACTCCA 1884

Qy 3986 GCATGAGATCCCGCGTGGAGGATCATCCAGCCGGCGTCCCGGAAAACGATTCCGAAGC 4045
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1883 GCATGAGATCCCGCGTGGAGGATCATCCAGCCGGCGTCCCGGAAAACGATTCCGAAGC 1824

Qy 4046 CCAACCTTTCATAGAAGGCGGGCCGGTGGAATCGAAATCGTGATGGCAGGTTGGGCGTCG 4105
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1823 CCAACCTTTCATAGAAGGCGGGCCGGTGGAATCGAAATCGTGATGGCAGGTTGGGCGTCG 1764

Qy 4106 CTTGGTCGGTCATTTCGAACCCCAGAGTCCCGCTCAGAAGAACTCGTCAAGAGGCGATA 4165
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1763 CTTGGTCGGTCATTTCGAACCCCAGAGTCCCGCTCAGAAGAACTCGTCAAGAGGCGATA 1704

Qy 4166 GAAGGCGATGCGCTGCGAATCGGGAGCGGCGGCGATACCGTAAAGCACAGAAGCGGTCAGC 4225
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1703 GAAGGCGATGCGCTGCGAATCGGGAGCGGCGGCGATACCGTAAAGCACAGAAGCGGTCAGC 1644

Qy 4226 CCAATTCGCCGCCAAGCTCTTCAGCAATATCACGGGTAGCCAACGCTATGTCCTGATAGCG 4285
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Db 1643 CCAATTCGCCGCCAAGCTCTTCAGCAATATCACGGGTAGCCAACGCTATGTCCTGATAGCG 1584

Qy 4286 GTCCGCCACACCCAGCCCGGCCACAGTCGATGAATCCAGAAAAGCGGCCATTTTCCACCAT 4345
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Db 1583 GTCCGCCACACCCAGCCCGGCCACAGTCGATGAATCCAGAAAAGCGGCCATTTTCCACCAT 1524

Qy 4346 GATATTCGGCAAGCAGGCATCGCCATCGGTCACGACCAGAATCCTCGCGTCGGGCATGCG 4405
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Db 1523 GATATTCGGCAAGCAGGCATCGCCATCGGTCACGACCAGAATCCTCGCGTCGGGCATGCG 1464

Qy 4406 CGCCTTGAGCCTGGCGAACAGTTCGGCTCGGCGCGAGCCCTGATGCTCTTCGTCCAGATC 4465
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1463 CGCCTTGAGCCTGGCGAACAGTTCGGCTCGGCGCGAGCCCTGATGCTCTTCGTCCAGATC 1404

Qy 4466 ATCCTGATCGACAAGACCGGCTTCCATCCGAGTACGTGCTCGCTCGATGATGTTTCGC 4525
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1403 ATCCTGATCGACAAGACCGGCTTCCATCCGAGTACGTGCTCGCTCGATGATGTTTCGC 1344

Qy 4526 TTGGTGGTCGAATGGGCAGGTAGCCGATCAAGCGTATGCAGCCGCGCATTGCATCAGC 4585
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1343 TTGGTGGTCGAATGGGCAGGTAGCCGATCAAGCGTATGCAGCCGCGCATTGCATCAGC 1284

Qy 4586 CATGATGGATACTTTCTCGGCGAGCAAGGTGAGATGACAGGAGATCCTGCCCCGGCAC 4645
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Db 1283 CATGATGGATACTTTCTCGGCGAGCAAGGTGAGATGACAGGAGATCCTGCCCCGGCAC 1224

Qy 4646 TTCGCCCAATAGCAGCCAGTCCCTTCCGGCTTCAGTGACAACGTCGAGCAACACGTTGCCA 4705
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1223 TTCGCCCAATAGCAGCCAGTCCCTTCCGGCTTCAGTGACAACGTCGAGCAACACGTTGCCA 1164

Qy 4706 AGGAACGGCCCGTCGTGCCGCAGCCACGATAGCCGCCGCCTCGTCCAGTTCATTCAG 4765
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Db 1163 AGGAACGGCCCGTCGTGCCGCAGCCACGATAGCCGCCGCCTCGTCCAGTTCATTCAG 1104

Qy 4766 GGCACCGGACAGGTCGGTCTTGACAAAAAGAACCGGGCGCCCTGCGCTGACAGCCGGAA 4825
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1103 GGCACCGGACAGGTCGGTCTTGACAAAAAGAACCGGGCGCCCTGCGCTGACAGCCGGAA 1044

Qy 4826 CACGGGCGGCATCAGAGCAGCCGATTGTCTGTTGTGCCCAGTCATAGCCGAATAGCCTCTC 4885
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1043 CACGGGCGGCATCAGAGCAGCCGATTGTCTGTTGTGCCCAGTCATAGCCGAATAGCCTCTC 984

Qy 4886 CACCCAAGCGGCCGGAGAACTGCGTGCAATCATCTTGTTCAATCATGCGAAACGATCC 4945
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Db 983 CACCCAAGCGGCCGGAGAACTGCGTGCAATCATCTTGTTCAATCATGCGAAACGATCC 924

Qy 4946 TCATCCTGTCTCTTGATCAGATCTTGATCCCTCGCGCCATCAGATCCTTGGCGCCAAGAA 5005
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Db 923 TCATCCTGTCTCTTGATCAGATCTTGATCCCTCGCGCCATCAGATCCTTGGCGCCAAGAA 864

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Db 863 AGCCATCCAGTTTACTTTGCAGGCTTCCAACCTTACCAGAGGGCGCCCAGCTGGCAA 804

Qy 5066 TTCCGGTTCGCTTGCTGTCCATAAAACCGGCCTCAGCTATCGCCATGTAAGCCACT 5125
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Db 803 TTCCGGTTCGCTTGCTGTCCATAAAACCGGCCTCAGCTATCGCCATGTAAGCCACT 744

Qy 5126 GCAAGCTACCTGCTTCTTCTTTTGCGCTTGGCTTGCCGTTTCCCTTGCGTTTCCAGTAGCT 5185
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Db 743 GCAAGCTACCTGCTTCTTCTTTTGCGCTTGGCTTGCCGTTTCCCTTGCGTTTCCAGTAGCT 684

Qy 5186 GACATTCATCCGGGGTCAGCACCGTTTCTGCGGACTGGCTTTCTACGTGTTCCGCTTCCT 5245
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Db 683 GACATTCATCCGGGGTCAGCACCGTTTCTGCGGACTGGCTTTCTACGTGTTCCGCTTCCT 624

Qy 5246 TTAGCAGCCCTTGCGCCCCTGAGTGCTTGCGGCAGCGTG 5283
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Db 623 TTAGCAGCCCTTGCGCCCCTGAGTGCTTGCGGCAGCGTG 586

RESULT 5
LOCUS   SYNCCDBB/c
DEFINITION   Cloning vector pKIL119 ccdB gene, complete cds and
               kanamycin-resistance gene (KmR) gene fragment.
ACCESSION   L38499
VERSION   L38499.1   GI:986979
KEYWORDS   ccdB gene; kanamycin resistance.
SOURCE   Cloning vector pKIL119
  ORGANISM   Cloning vector pKIL119
               other sequences; artificial sequences; vectors.
REFERENCE   1 (bases 1 to 2999)
  AUTHORS   Bernard,P.
  TITLE   New ccdB positive-selection cloning vectors with kanamycin or
               chloramphenicol selectable markers
  JOURNAL   Gene 162 (1), 159-160 (1995)
  MEDLINE   96009896
  PUBMED   7557407
FEATURES   Location/Qualifiers
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     gene   1..381
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                     /db_xref="GI:986980"
                     /translation="MTMITPSLHACRSTLEDPRVPSSNSLQFKVYTYKESRYRLFVD
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                     EEVADLSHRENDIKNAINLMFWGI"

ORIGIN

Query Match   42.0%;   Score 2218.4;   DB 12;   Length 2999;
Best Local Similarity   93.4%;   Pred. No. 0;
Matches 2388;   Conservative   0;   Mismatches   26;   Indels   144;   Gaps   1;

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Qy  2726 AGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCCACACAACATACGAGCCGGAA 2785
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Db  2999 AGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCCACACAACATACGAGCCGGAA 2940

Qy  2786 GCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACATTAATTGCGTTGC 2845
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Db  2939 GCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACATTAATTGCGTTGC 2880

Qy  2846 GCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCATTAATGAATCGGCC 2905
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Db  2879 GCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCATTAATGAATCGGCC 2820

Qy  2906 AACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTTCCTCGCTCACTGACT 2965
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Db  2819 AACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTTCCTCGCTCACTGACT 2760

Qy  2966 CGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCAAAGGCGGTAATAC 3025
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Db  2759 CGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCAAAGGCGGTAATAC 2700

Qy  3026 GGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCAAAAGGCCAGCAAA 3085
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2699 GGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCAAAAGGCCAGCAAA 2640

Qy  3086 AGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCCTG 3145
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Db  2639 AGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCCTG 2580

Qy  3146 ACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAA 3205
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2579 ACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAA 2520

Qy  3206 GATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGC 3265
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2519 GATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGC 2460

Qy  3266 TTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCAC 3325
         |||||||||||||||||||||||||||||||||||||||||||||||||||||   |||||
Db  2459 TTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCAATGCTCAC 2400

Qy  3326 GCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTGCACGAAC 3385
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Db  2399 GCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTGCACGAAC 2340

Qy  3386 CCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGG 3445
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Db  2339 CCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGG 2280

Qy  3446 TAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGT 3505
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Db  2279 TAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGT 2220

Qy  3506 ATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAA 3565
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Db  2219 ATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGGA 2160

Qy  3566 CAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCT 3625
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Db  2159 CAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCT 2100

Qy  3626 CTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTTTGCAAGCAGCAGA 3685
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Db  2099 CTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTTTGCAAGCAGCAGA 2040

Qy  3686 TTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACG 3745
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Db  2039 TTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACG 1980

Qy  3746 CTCAGTGGAACGAAAACTCACGTTAAGGGATTTTGGTCATGAGATTATCGTCGACCAAAG 3805
         |||||||||||||||||||||||||||||||||||||||||||||||||           
Db  1979 CTCAGTGGAACGAAAACTCACGTTAAGGGATTTTGGTCATGAGATTATCAAAAAGATCT 1920


Qy  3806 CGGCCATCGTGCCTCCCACTCCTGCAGTTCGGCGGCATGATGCGGATAGCCGCTGC 3865
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Db  1906 TCACCTTAGATCCTT 1919

Qy  3866 TGGTTTCCTGGATGCCGACGGATTTGCACTGCCGGTAGAACTCCGCGAGGTCGTCCAGCC 3925
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Qy  3926 TCAGGCAGCAGTGAACCAACTCGCGAGGGGGATCGAGCCCCGGGGTGGGCGAAGAACTCCA 3985
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Db  1905 --------------------------------TTTGGGGTGGGCGAAGAACTCCA 1884

Qy  3986 GCATGAGATCCCGCGCTGGAGGATCATCCAGCCGCGTCCGGAAAACGATTCCGAAGC 4045
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Db  1883 GCATGAGATCCCGCGCTGGAGGATCATCCAGCCGCGTCCGGAAAACGATTCCGAAGC 1824

Qy  4046 CCAACCTTTCATAGAAGGCGCGGTGGAATCGAAATCTCGTGATGGCAGGTTGGGCGTCG 4105
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Db  1823 CCAACCTTTCATAGAAGGCGCGGTGGAATCGAAATCTCGTGATGGCAGGTTGGGCGTCG 1764

Qy  4106 CTTGGTCGGTCATTTGAACCGCTGCTCAGAGTCCCGCTCAGAAGAACTCGTCAAGAAGGCGATA 4165
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1763 CTTGGTCGGTCATTTGAACCGCTGCTCAGAGTCCCGCTCAGAAGAACTCGTCAAGAAGGCGATA 1704

Qy  4166 GAAGGCGATGGCGTGGAATCGCGATACCGGTGCATACCGTAAAGCACGAGGAAGCGGTCAGC 4225
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1703 GAAGGCGATGGCGTGGAATCGCGATACCGGTGCATACCGTAAAGCACGAGGAAGCGGTCAGC 1644

Qy  4226 CCATTCGCCGCCAAGCTCTTCAGCAATATCACGGGTAGCCAACGCTATGTCCTGATAGCG 4285
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1643 CCATTCGCCGCCAAGCTCTTCAGCAATATCACGGGTAGCCAACGCTATGTCCTGATAGCG 1584

Qy  4286 GTCCGCCACACCCAGCCGGCCACAGTCGATGAATCCAGAAAAGCGGCCATTTTCCACCAT 4345
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Db  1583 GTCCGCCACACCCAGCCGGCCACAGTCGATGAATCCAGAAAAGCGGCCATTTTCCACCAT 1524

Qy  4346 GATATTCGGCAAGCAGGCATCGCCATGGGTCACGACGAGATCCTCGCCGTCGGGCATGCG 4405
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1523 GATATTCGGCAAGCAGGCATCGCCATGGGTCACGACGAGATCCTCGCCGTCGGGCATGCG 1464

Qy  4406 CGCCTTGAGCCTGGCGAACAGTTCGGCTGGCGCGAGCCCCTGATGCTCTTCGTCCAGATC 4465
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Db  1463 CGCCTTGAGCCTGGCGAACAGTTCGGCTGGCGCGAGCCCCTGATGCTCTTCGTCCAGATC 1404

Qy  4466 ATCCTGATCGACAAGACCGGCTTCCATCCGAGTACGTGCTCGCTCGATGCGATGTTTCGC 4525
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1403 ATCCTGATCGACAAGACCGGCTTCCATCCGAGTACGTGCTCGCTCGATGCGATGTTTCGC 1344

Qy  4526 TTGGTGTCGAATGGGCAGGTAGCCGGATCAAGCGTATGCAGCCGCCGCATTGCATCAGC 4585
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1343 TTGGTGTCGAATGGGCAGGTAGCCGGATCAAGCGTATGCAGCCGCCGCATTGCATCAGC 1284

Qy  4586 CATGATGGATACTTTCTCGGCAGGAGCAAGGTGAGATGACAGGAGATCCTGCCCCGGCAC 4645
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Db  1283 CATGATGGATACTTTCTCGGCAGGAGCAAGGTGAGATGACAGGAGATCCTGCCCCGGCAC 1224

Qy  4646 TTCGCCCAATAGCAGCCAGTCCCTTCCCGCTTCAGTGACAACGTCGAGCACAGCTGCGCA 4705
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Db  1223 TTCGCCCAATAGCAGCCAGTCCCTTCCCGCTTCAGTGACAACGTCGAGCACAGCTGCGCA 1164

Qy  4706 AGGAACGCCCGTCGTGGCCAGCCACGATAGCCGCGCTGCCTCGTCCTGCAGTTCATTCAG 4765
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Db  1163 AGGAACGCCCGTCGTGGCCAGCCACGATAGCCGCGCTGCCTCGTCCTGGAGTTCATTCAG 1104

Qy  4766 GGCACCGGACAGGTCGGTCTTGACAAAAAGAACCGGGCGCCCCTGCGCTGACAGCCGGAA 4825
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Db  1103 GGCACCGGACAGGTCGGTCTTGACAAAAAGAACCGGGCGCCCCTGCGCTGACAGCCGGAA 1044

Qy  4826 CACGGGCGGCATCAGCAGCCCAGTTGTGTGCCCCAGTCATAGCCGAATAGCCTCTC 4885
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Db  1043 CACGGGCGGCATCAGCAGCCCAGTTGTGTGCCCCAGTCATAGCCGAATAGCCTCTC 984

Qy  4886 CACCCAAGCGGCCGGAGAACCTGCGTGCAATCATCTTGTTCAATCATGCGAAACGATCC 4945
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Db    983 CACCCAAGCGGCCGGAGAACCTGCGTGCAATCCATCTTGTTCAATCATGCGGAAACGATCC  924
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Qy   2424 ACCTGTCTGCGCAGCTGCATTAATGAATCGGCCAACGGCGGGGGAGAGGCGGTTTGCGTA 2365

Qy   4946 TCATCCTGTCTCTTGATCAGATCTTGATCCGTGCGCCATCAGATCCTTGGCGCGGCAGAA 5005
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Db    923 TCATCCTGTCTCTTGATCAGATCTTGATCCGTGCGCCATCAGATCCTTGGCGCGGCAGAA  864
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Db   2933 TTGGGCGGTCTTCCGCTTCCTGCCTCTCACTGACTCGGTCGTTCGGCTGCGGC 2992

Qy   5006 AGCCATCCAGTTTACTTTGCAGGGCTTCCCAACCTTACCAGAGAGGCGCCCCAGTCGGCAA 5065
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    863 AGCCATCCAGTTTACTTTGCAGGGCTTCCCAACCTTACCAGAGAGGCGCCCCAGTCGGCAA  804
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2993 GAGCGGTATCAGCTCACTCAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACG 3052

Qy   5066 TTCCGGTTCGCTTGCTGTCATAAAACCGCCAGTCGTAGCTAGCTATCGCCATGTAAGCCCACT 5125
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    803 TTCCGGTTCGCTTGCTGTCGTCCATAAAACCGCCAGTCGTAGCTAGCTATCGCCATGTAAGCCCACT  744
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Db   3053 CAGGAAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCT 3112

Qy   5126 GCAAGCTACCTGCTTTCTCTTTGCCGCTTGGCGTTTCCCTTGTCCAGATAGCCCAGTAGCT 5185
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Db    743 GCAAGCTACCTGCTTTCTCTTTGCCGCTTGGCGTTTCCCTTGTCCAGATAGCCCAGTAGCT  684
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Db   3113 TGCTGGCGTTTTTCCATAGGCTCCGCCCCCCTGTCGAGCATCACAAAATCGACGCTCA 3172

Qy   5186 GACATTCATCCGGGGTCAGCACCGTTTCTGCGGACTGGCTTTCTACGTGTTCCGCTTCCT 5245
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    683 GACATTCATCCGGGGTCAGCACCGTTTCTGCGGACTGGCTTTCTACGTGTTCCGCTTCCT  624
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3173 GTCAGAGGTGGCGAAACCCGACACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCT 3232

Qy   5246 TTAGCAGCCCTTGCGCCCTGAGTGCTTGCGGGCAGCGTG 5283
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Db    623 TTAGCAGCCCTTGCGCCCTGAGTGCTTGCGGGCAGCGTG  586
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Db   3233 CCCTCGTGCGCTCCTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCC 3292

Qy   3293 CTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGG 3352
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Db   2004 CTTCGGGAAGCGTGGCGCTTTCTCAATGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGG 1945

Qy   3353 TCGTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCGTTCAGCCCGACCGCTGCGCCTT 3412
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1944 TCGTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCGTTCAGCCCGACCGCTGCGCCTT 1885

Qy   3413 TATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACAGACTTATCGCCACTGGCAG 3472
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1884 TATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACAGACTTATCGCCACTGGCAG 1825

Qy   3473 CAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGA 3532
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1824 CAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGA 1765

Qy   3533 AGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTGGTATCTGCGCTCTGCTGA 3592
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Db   1764 AGTGGTGGCCTAACTACGGCTACACTAGAAGGACAGTATTTGGTATCTGCGCTCTGCTGA 1705

Qy   3593 AGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTG 3652
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Db   1704 AGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTG 1645

Qy   3653 GTAGCGGTGGTTTTTTTGTTTGCAAGCAGCAGATTACGGCGCAGAAAAAAAGGATCTCAAG 3712
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Qy   3713 AAGATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGGAACGAAAACTCACGTTAAG 3772
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Db   1584 AAGATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGGAACGAAAACTCACGTTAAG 1525

Qy   3773 GGATTTTGGTCATGAGATTATCGTCGACCAAAGCGGCCATCGTGCCTCGCCACTCCTGCA 3832
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Db   1524 GGATTTTGGTCATGAGATTATCAAAAGGATCTTCACCTAGATCCTT---------------- 1478

Qy   3833 GTTCGGGGGCATGGATGACGCGGATAGCCGCTGCTGGTTTCCTGGATGCCGACGGGATTTGC 3892
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Db   1477 ------------------------------------------------------------ 1477

Qy   3893 ACTGCCGGTAGAACTCCGCGAGGTCGTCCAGCCTCCAGGCAGCAGCTGAACCAACTCGCGA 3952
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Db   1477 ------------------------------------------------------------ 1477

Qy   3953 GGGGATCGAGCCCGGGGTGGGCAGCATGAAGAACTCCAGCATGCATGAGATCCCGGCTGGAGGATCA 4012
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RESULT 6
AY189826/c

LOCUS   AY189826   2604 bp   DNA   circular SYN 09-APR-2003
DEFINITION His-3 integration vector pJHAM001, complete sequence.
ACCESSION   AY189826
VERSION   AY189826.1 GI:28435536
KEYWORDS   .
SOURCE   his-3 integration vector pJHAM001
  ORGANISM his-3 integration vector pJHAM001
            other sequences; artificial sequences; vectors.
REFERENCE   1 (bases 1 to 2604)
  AUTHORS   Lee,D.W. Haag,J.R. and Aramayo,R.
  TITLE   Construction of strains for rapid homokaryon purification after
            integration of constructs at the histidine-3 (his-3) locus of
            Neurospora crassa
  JOURNAL   Curr. Genet. 43 (1), 17-23 (2003)
   PUBMED   12684841
REFERENCE   2 (bases 1 to 2604)
  AUTHORS   Lee,D.W., Haag,J.R. and Aramayo,R.
  TITLE   Direct Submission
  JOURNAL   Submitted (03-DEC-2002) Biology, Texas A&M University, BSBW 415,
            College Station, TX 77843-3258, USA
FEATURES   Location/Qualifiers
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                     /organism="his-3 integration vector pJHAM001"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:220724"
                     /note="modified pKI8 vector"
     misc_feature   2542..2572
                     /note="modified multi-cloning site"
ORIGIN

Query Match   41.2%; Score 2177.4; DB 12; Length 2604;
Best Local Similarity   93.2%; Pred. No. 0;
Matches 2359; Conservative   0; Mismatches   26; Indels   146; Gaps   2;

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Qy   2753 CGCTCACAATTCCACACAACATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCT 2812
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Db   2542 CGCTCACAATTCCACACAACATA--AGCCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCT 2485

Qy   2813 AATGAGTGAGCTAACTCACATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAA 2872
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Db   2484 AATGAGTGAGCTAACTCACATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAA 2425

Qy   2873 ACCTGTCTGCGCAGCTGCATTAATGAATCGGCCAACGGCGGGGAGAGGCGGTTTGCGTA 2932
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Db   5093 CGCCCAGTCTAGCTATCGCCATGTAAGCCACTGCTTCTCCTTTGCGCT 5152
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Qy    348 CGCCCAGTCTAGCTATCGCCATGTAAGCCCACTGCTTCTCCTTTGCGCT  289

Db   5153 TGCGTTTTCCCTTGTCCAGATAGCCCAGTAGCTGCTGACAATTCATCCG 5212
          ||||||||||||||||||||||||||||||||||||||||||||||||| 
Qy    288 TGCGTTTTCCCTTGTCCAGATAGCCCAGTAGCTGCTGACAATTCATCCG  229

Db   5213 CTGCGGACTGCTTTTCTACGTGTTCCGCTTCCTTTAGCACGCCCTTGCG 5272
          |||||||||||||||||||||||||||||||||||||||||||||||||
Qy    228 CTGCGGACTGCTTTTCTACGTGTTCCGCTTCCTTTAGCACGCCCTTGCG  169

Db   5273 GCGGCAGCGTG 5283
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Qy    168 GCGGCAGCGTG  158
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RESULT 7
AY189827/c

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LOCUS       AY189827               11373 bp    DNA     circular SYN 09-APR-2003
DEFINITION  His-3 integration vector pJHAM002, complete sequence.
ACCESSION   AY189827
VERSION     AY189827.1  GI:28435537
KEYWORDS    .
SOURCE      his-3 integration vector pJHAM002
  ORGANISM  his-3 integration vector pJHAM002
            other sequences; artificial sequences; vectors.
REFERENCE   1  (bases 1 to 11373)
  AUTHORS   Lee,D.W., Haag,J.R. and Aramayo,R.
  TITLE     Construction of strains for rapid homokaryon purification after
            integration of constructs at the histidine-3 (his-3) locus of
            Neurospora crassa
  JOURNAL   Curr. Genet. 43 (1), 17-23 (2003)
  PUBMED    12684841
REFERENCE   2  (bases 1 to 11373)
  AUTHORS   Lee,D.W., Haag,J.R. and Aramayo,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (03-DEC-2002) Biology, Texas A&M University, BSBW 415,
            College Station, TX 77843-3258, USA
FEATURES             Location/Qualifiers
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     source          1..2597
                     /organism="his-3 integration vector pJHAM001"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:220724"
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     misc_feature    6156..6183
                     /note="multi-cloning sites"
ORIGIN
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Query Match             41.2%;  Score 2177.4;  DB 12;  Length 11373;
  Best Local Similarity   93.2%;  Pred. No. 0;
  Matches 2359;  Conservative    0;  Mismatches   26;  Indels  146;  Gaps    2;

Qy   2753 CGCTCACAATTCCACACAACATACAGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCT 2812
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Db   2574 CGCTCACAATTCCACACAACAACATA--AGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCT 2517

Qy   2813 AATGAGTGAGCTAACTCACATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAA 2872
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2516 AATGAGTGAGCTAACTCACATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAA 2457

Qy   2873 ACCTGTCGTGCCAGCTGCATTAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTA 2932
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| 
Db   2456 ACCTGTCGTGCCAGCTGCATTAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTA 2397

Qy   2933 TTGGGCGCTCTTCCGCTTCCTCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGC 2992
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Db   1477 ----------TTGGGGTGGCGAAGAACTCCAGCATGAGATCCCCGCGCTGGAGGATCA 1429
                    |||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4013 TCCAGCCGGGCGTCCCCGGAAAAACGATTCCGAAGCCCAACCTTTCATAGAAGGCGGCGGTGG 4072
          ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db   1428 TCCAGCCGGGCGTCCCGGAAAAACGATTCCGAAGCCCAACCTTTCATAGAAGGCGGCGGTGG 1369

Qy   4073 AATCGAAATCTCGTGATGGCAGGTTGGGCGTCGCTTGGTCGGTCATTTCGAACCCCAGAG 4132
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| 
Db   1368 AATCGAAATCTCGTGATGGCAGGTTGGGCGTCGCTTGGTCGGTCATTTCGAACCCCAGAG 1309

Qy   4133 TCCCGCTCAGAAGAACTCGTCAAGAAGGCGATAGAAGGCGATGCGCTGCGAATCGGGAGC 4192
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| 
Db   1308 TCCCGCTCAGAAGAACTCGTCAAGAAGGCGATAGAAGGCGATGCGCTGCGAATCGGGAGC 1249

Qy   4193 GGCGATACCGTAAAGCACGAGGAAGCGGTCAGCCCATTCGCCGCCAAGCTCTTCAGCAAT 4252
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| 
Db   1248 GGCGATACCGTAAAGCACGAGGAAGCGGTCAGCCCATTCGCCGCCAAGCTCTTCAGCAAT 1189

Qy   4253 ATCACGGGTAGCCAACGCTATGTCCTGATAGCGGTCCGATAGCGGTCCGCCACACCCCAGTC 4312
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| 
Db   1188 ATCACGGGTAGCCAACGCTATGTCCTGATAGCGGTCCGATAGCGGTCCGCCACACCCCAGTC 1129

Qy   4313 GATGAATCCAGAAAAGCGGCCATTTTCCACCATGATATTCGGCAAGCAGGCATCGCCATG 4372
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| 
Db   1128 GATGAATCCAGAAAAGCGGCCATTTTCCACCATGATATTCGGCAAGCAGGCATCGCCATG 1069

Qy   4373 GGTCACGACGAGATCCTCGCCGTCGGGCATGCGCGCCTTGAGCCTGGCGAACAGTTCGGC 4432
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| 
Db   1068 GGTCACGACGAGATCCTCGCCGTCGGGCATGCGCGCCTTGAGCCTGGCGAACAGTTCGGC 1009

Qy   4433 TGGCGCGAGCCCCTGATGCTCTTCGTCCAGATCATCCTGATCGACAGACCGGCTTCCAT 4492
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Db   1008 TGGCGCGAGCCCCTGATGCTCTTCGTCCAGATCATCCTGATCGACAGACCGGCTTCCAT  949

Qy   4493 CCGAGTACGTGCTCGCTCGATGCGATGTTTCGCTTGGTGGTGTCGAATGGGCAGGTAGCCGG 4552
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   4553 ATCAAGCTATGCAGCCGCCGCATTGCATCAGCCATGATGATACTTTCTCGGCAGGAGC 4612
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| 
Db    888 ATCAAGCTATGCAGCCGCCGCATTGCATCAGCCATGATGATACTTTCTCGGCAGGAGC  829

Qy   4613 AAGGTGAGATGACAGGAGATCCTGCCCCGGCACTTCGCCCAATAGCAGCCAGTCCCTTCC 4672
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Qy   4673 CGCTTCAGTGACAACGTCGAGCACAGCTGCGCAAGGAACGCCCGTCGTGGCCAGCCACGA 4732
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Qy   4733 TAGCCGGCGTGCTCGTCCTGCAGTTCATTCAGGGCACCGGACAGGTCGGTCTTGACAAA 4792
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Qy   4793 AAGAACCGGGCGCCCGGCGCCCCTGCGCTGACAGCCGGAACACACGGCGGCCATCAGAGCCGATTGT 4852
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    648 AAGAACCGGGCGCCCGGCGCCCCTGCGCTGACAGCCGGAACACACGGCGGCCATCAGAGCCGATTGT  589

Qy   4853 CTGTTGTGCCCAGTCATAGCCGAATAGCCTCCCACCCACCCGGAACCTGCGTG 4912
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   4913 CAATCCATCTTGTTCAATCATGCGAAACGATCTCATCCTGTCTCTTGATCAGATCTTGA 4972
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db    468 TCCCCTGCGCCATCAGATCTTGGGCGGCAAGAAAGCCATCCAGTTTACTTTGCAGGGCTT  409

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          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| 
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Db   2396 ||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   2993 GAGGCGTATCAGCTCACTCAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACG 3052
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Qy   3413 TATCCGGTAACTAACTACGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAG 3472
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Db   1510 ----------------------------------------------------------- 1510

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Db   1509 -----------TTGGGGTGGGCGAAGAACTTCCAGCATGCGCGCTGGAGGATCA 1461

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Qy   4733 TAGCCGCGCTGCCTCGTCATTCAGGTCATTCAGGGCACCGGACAGGTCGGTCTTGACAAA 4792
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Qy   4913 CAATCCATCTTGTTCAATCATGCGAAACGATCCTCGTCTCTTGATCAGATCTTGA 4972
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Db   560  CAATCCATCTTGTTCAATCATGCGAAACGATCCTCGTCTCTTGATCAGATCTTGA 501

Qy   4973 TCCCCTGCGCCATCAGATCCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTGCAGGGCTT 5032
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Qy   5093 CGCCCAGTCTAGCTATCGCCATGTAAGCCCACTGCAAGCTACCTGCTTTCTCTTTGCGCT 5152
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Qy  5153  TGCGTTTTCCCTTGTCCAGATAGCCCAGTAGCTTGACATTCATCCGGGGTCAGCACCGTTT  5212
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Db   320  TGCGTTTTCCCTTGTCCAGATAGCCCAGTAGCTTGACATTCATCCGGGGTCAGCACCGTTT   261

Qy  5213  CTGCGGACTGGCTTTCTACGTGTTCCGCTTCCTTTAGCAGCCCCTTGCGCCCTGAGTGCTT  5272
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Db   260  CTGCGGACTGGCTTTCTACGTGTTCCGCTTCCTTTAGCAGCCCCTTGCGCCCTGAGTGCTT   201

Qy  5273  GCGGCAGCGTG  5283
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RESULT 8
AY189829/c

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DEFINITION  His-3 integration vector pJHAM004, complete sequence.
ACCESSION   AY189829
VERSION     AY189829.1  GI:28435539
KEYWORDS    .
SOURCE      his-3 integration vector pJHAM004
  ORGANISM  his-3 integration vector pJHAM004
            other sequences; artificial sequences; vectors.
REFERENCE   1  (bases 1 to 11403)
  AUTHORS   Lee,D.W., Haag,J.R. and Aramayo,R.
  TITLE     Construction of strains for rapid homokaryon purification after
            integration of constructs at the histidine-3 (his-3) locus of
            Neurospora crassa
  JOURNAL   Curr. Genet. 43 (1), 17-23 (2003)
   PUBMED   12684841
REFERENCE   2  (bases 1 to 11403)
  AUTHORS   Lee,D.W., Haag,J.R. and Aramayo,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (03-DEC-2002) Biology, Texas A&M University, BSBW 415,
            College Station, TX 77843-3258, USA
FEATURES             Location/Qualifiers
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                     /note="multi-cloning sites"
ORIGIN

Query Match             41.2%;  Score 2177.4;  DB 12;  Length 11403;
  Best Local Similarity   93.2%;  Pred. No. 0;
  Matches 2359;  Conservative    0;  Mismatches   26;  Indels 146;  Gaps  2;
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Qy  2336  GAGCGGTATCAGCTCACTCAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACG  2277
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Qy  3053  CAGGAAAGAACATGTGAGCAAGAGGCAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGT  3112
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Db  2276  CAGGAAAGAACATGTGAGCAAGAGGCAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGT  2217

Qy  3113  TGCTGGCGTTTTTCCATAGGCTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAA  3172
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Qy  3173  GTCAGAGGTGGCGAAACCCGACACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCT  3232
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Qy  3233  CCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCC  3292
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Qy  3353  TCGTTGCTCCAAGCTGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTT  3412
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Qy  3893  ACTGCCGGTAGCTCCGCGAGGTCGTCCAGCCTCGTCCGGCCAGCTGAACCAACTCGCGA  3952
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Db  1509  --------TTGGGGTGGGCCGTCCCCGGAAAACGATTCCGAAGCCCAACCTTTCATAGAAGGCGGCGGTGG  1461

Qy  4013  TCCAGCCGGTCGGCGTCCCGAAAACGATTCCGAAGCCCAACCTTTCATAGAAGGCGGTGG  4072
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Qy  2993  GAGCGGTATCAGCTCACTCAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACG  3052
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Qy  2753  CGCTCACAATTCCACACAACATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCT  2812
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Db  2574  CGCTCACAATTCCACACAACATA--AGCCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCT  2517

Qy  2813  AATGAGTGAGCTAACTCACATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAA  2872
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Qy  2933  TTGGGCGCTCTTCCGCTTCCTCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGC  2992
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ACCESSION   AY222815
VERSION   AY222815.1 GI:29242889
KEYWORDS   .
SOURCE   Cloning vector pKl9mob2
  ORGANISM Cloning vector pKl9mob2
            other sequences; artificial sequences; vectors.
REFERENCE   1 (bases 1 to 3036)
  AUTHORS   Kirchner,O. and Tauch,A.
  TITLE   Tools for genetic engineering in the amino acid-producing bacterium
            Corynebacterium glutamicum
  JOURNAL   J. Biotechnol. 104 (1-3), 287-299 (2003)
   MEDLINE   22830032
   PUBMED   12948646
REFERENCE   2 (bases 1 to 3036)
  AUTHORS   Kirchner,O. and Tauch,A.
  TITLE   Direct Submission
  JOURNAL   Submitted (22-JAN-2003) Department of Genetics, University of
            Bielefeld, Universitaetsstrasse 25, Bielefeld D-33615, Germany
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Qy   2949  TTCCTCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGCTCA  3008
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Db   2970  TTCCTCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGCTCA  2911

Qy   3009  CTCAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTG  3068
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Qy   3069  AGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCA  3128
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Qy   3129  TAGGCTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAA  3188
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Db   2790  TAGGCTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAA  2731

Qy   3189  CCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCC  3248
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Qy   3249  TGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGC  3308
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Db   2670  TGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGC  2611

Qy   3309  GCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCT  3368
           |||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   3369  GGGCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCG  3428
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Db   2550  GGGCTGTGTGCACGAACCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCG   2491

Qy   3429  TCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAG  3488
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Db   2430  GATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTA  2371

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Db   2370  CGGCTACACTAGAAGGACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGG  2311

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RESULT 10
AY219859/c
LOCUS       AY219859                3210 bp    DNA     circular SYN 05-SEP-2003
DEFINITION  Cloning vector pK19MECA2, complete sequence.
ACCESSION   AY219859
VERSION     AY219855.1  GI:29164979
KEYWORDS    .
SOURCE      Cloning vector pK19MECA2
  ORGANISM  Cloning vector pK19MECA2
            other sequences; artificial sequences; vectors.
REFERENCE   1  (bases 1 to 3210)
  AUTHORS   Kirchner,O. and Tauch,A.
  TITLE     Tools for genetic engineering in the amino acid-producing bacterium
            Corynebacterium glutamicum
  JOURNAL   J. Biotechnol. 104 (1-3), 287-299 (2003)
   MEDLINE  22830032
   PUBMED   12948646
REFERENCE   2  (bases 1 to 3210)
  AUTHORS   Kirchner,O. and Tauch,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-JAN-2003) Department of Genetics, University of
            Bielefeld, Universitaetsstrasse 25, Bielefeld D-33615, Germany
FEATURES             Location/Qualifiers
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Qy 4518 TGTTTCGCTTGGTGGTCGAATGGGCAGGTAGCGATGCCGATCAAGCGTATGCAGCCGCCGCATT 4577
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Db 1170 TGTTTTGCTTGGTCGAATGGGCAGGTAGCCGGATCAAGCGTATGCAGCCGCCGCCGCCGCATT 1111

Qy 4578 GCATCAGCCATGATGATGACTTCTCCGGAGGAGCAAGGTGAGATGACAGAGAGATCCTGC 4637
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Db 1110 GCATCAGCCATGATGATGACTTCTCCGGAGGAGCAAGGTGAGATGACAGAGAGATCCTGC 1051

Qy 4638 CCCGGCACTTCGCCAATAGCAGCCAGTCCCTTCCGGCTTCAGTGACAACGTCGAGCACA 4697
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Db 1050 CCCGGCACTTCGCCCAATAGCAGCCAGTCCCTTCCGGCTTCAGTGACAACGTCGAGCACA 991

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Db 990 GCTGCGCAAGGAACGCCCGTCGTGGCCAGCCACGATAGCCGCACGATAGCCCGTCGTCTTGGAGT 931

Qy 4758 TCATTCAGGGCACCGGACAGCTCGGTCTTGACAAAAGAACCGCCGCCCCTCGCTGAC 4817
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Db 870 AGCCGGAACACGGCGGCATCAGAGACAGCCCAGTTGTCTGTTGTGTGCCCAGTCATAGCCGAAT 811

Qy 4878 AGCCTCTCCACCCAAGCGGCCGGAGAACCTGCGTGCGAATCCATCTTGTTCAATCATGCGA 4937
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Qy 4938 AACGATCCTCATCCTGTCTCTTGATCAGATCTTGATCTTGATCAGATCTTGGC 4997
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Qy 4998 GGCAAGAAAGCCATCCAGTTTACTTTGCAGGGCTTCCCAACCTTACCAGAGAGGGCGCCCCA 5057
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Db 690 GGCAAGAAAGCCATCCAGTTTACTTTGCAGGGCTTCCCAACCTTACCAGAGAGGGCGCCCCA 631

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Db 630 GCTGGCAATTCCGGTTCGCTTGCTGTCGTCGTCCATAAAACCGCCAGTCTAGCTATCGCCATGTA 571

Qy 5118 AGCCCACTGCAAGCTACCTGCTTCCTTGCGCTTGCGATGGCAGGTT 5177
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Db 570 AGCCCACTGCAAGCTACCTGCTTTCTTGCGCTTGCGATGGCAGGTT 511

Qy 5178 CAGTAGCTGACATTCATCCGGGGTCAGCACCGTTTCTGCGACTGGCTTTCTACGTGTTC 5237
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Db 510 CAGTAGCTGACATTCATCCGGGGTCAGCACCGTTTCTGCGACTGGCTTTCTACGTGTTC 451

Qy 5238 CGCTTCCTTTAGCAGCCCTTGCGCCCCTGAGTGCTTGCGGCAGCGTG 5283
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Db 450 CGCTTCCTTTAGCAGCCCTTGCGCCCCTGAGTGCTTGCGGCAGCGTG 405

RESULT 11
AY222822/c
LOCUS   AY222822   5695 bp   DNA   circular SYN 05-SEP-2003
DEFINITION   Shuttle vector pEC-K19mob2, complete sequence.
ACCESSION   AY222822
VERSION   AY222822.1 GI:29242905
KEYWORDS   .
SOURCE   Shuttle vector pEC-K19mob2
  ORGANISM   other sequences; artificial sequences; vectors.
             1 (bases 1 to 5695)
REFERENCE   Kirchner,O. and Tauch,A.
  AUTHORS   Tools for genetic engineering in the amino acid-producing bacterium
  TITLE   Corynebacterium glutamicum
  JOURNAL   J. Biotechnol. 104 (1-3), 287-299 (2003)
  MEDLINE   22830032
  PUBMED   12948646
REFERENCE   2 (bases 1 to 5695)

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Db 1830 AGGAAGGGCAGCCACCCTATCAAGGTGTACTGCCTTCAAGCGGTGTACTGCGCCTTCCAGAGAGCGGATTGAG 1771

Qy 4008 GATCATCCAGC----------- 4018
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Qy 4019 --------CGGCGTCCCGGAAAACGAT 4037
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Db 1650 TCCGAAGCCCCAACCTTTCATAGAAGGCGGCCGGTGGAATCGAAATCGTGATGGCAGGTT 1591

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AUTHORS   Kirchner,O. and Tauch,A.
TITLE     Direct Submission
JOURNAL   Submitted (22-JAN-2003) Department of Genetics, University of
          Bielefeld, Universitaetsstrasse 25, Bielefeld D-33615, Germany
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Query Match         39.5%;  Score 2088.4;  DB 12;  Length 5695;
Best Local Similarity  86.7%;  Pred. No. 0;
Matches  2434;  Conservative  0;  Mismatches  141;  Indels  231;  Gaps  3;

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Db   4675 TTCTACGGGGTCTGACGCTCAGTGGAACGAAAACTCACGTTAAGGGATTTTGGTCATGGC  4616

Qy   3789 ATTATCGTCG-------                                            3798
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Db   4615 TTTTCGGCTCATAACCCTGCTTCGGGGTCATTATAGCGATTTTTTCGGTATATCCATCC  4556

Qy   3799 ----------------                                            3798
Db   4555 TTTTTCGCACGATATACAGGATTTTGCCAAAGGGTTCGTGTAGACTTTCCTTGGTGTATC  4496

Qy   2709 GACGTAATCATGGTCATAGCTGTTTCCGTGTCGAAATTGTTATCCGCTCACAATTCCACA  2768
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Db   3415 TCATTCAGGGCACCGACACAGTCGGTCTTGACAAAAGAACCGGCGCCCTGCGCTGAC 3356

Qy   4818 AGCCGGAACACGCGGCCATCAGAGACGCCGATTGTCGTTGTGCCCAGTCATAGCCGAAT 4877
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Qy   4938 AACGATCCTATCCTGTCTCTTGATCAGATCTTGATCCCCTGCGCGCCATCAGATCCTTGGC 4997
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Qy   5178 CAGTAGCTGACATTCATCCGGGGTCAGCACCGTTTCTCGCGGACTGGCTTTCTACGTGTTTC 5237
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DEFINITION Shuttle vector pEC-K19MECA2, complete sequence.
ACCESSION   AY219861
VERSION   AY219861.1 GI:29164983
KEYWORDS   .
SOURCE   Shuttle vector pEC-K19MECA2
  ORGANISM Shuttle vector pEC-K19MECA2
            other sequences; artificial sequences; vectors.
REFERENCE   1 (bases 1 to 5869)
  AUTHORS   Kirchner,O. and Tauch,A.
  TITLE   Tools for genetic engineering in the amino acid-producing bacterium
            Corynebacterium glutamicum
  JOURNAL   J. Biotechnol. 104 (1-3), 287-299 (2003)
  MEDLINE   22830032
  PUBMED   12948646
REFERENCE   2 (bases 1 to 5869)
  AUTHORS   Kirchner,O. and Tauch,A.
  TITLE   Direct Submission
  JOURNAL   Submitted (15-JAN-2003) Department of Genetics, University of
            Bielefeld, Universitaetsstrasse 25, Bielefeld D-33615, Germany
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Qy   3948 CGCCGAGGGGATGCGAGCCCGGGGTGGCGAAGAACTCCAGCATGGAGATCCCCGGCCTGCGAG 4007
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Qy   4008 GATCATCCAGC----------- 4018
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Qy   4019 -----------------CGGCTGCCCGGAAAACGAT 4037
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Db   4075 GGGGCTGCGTCGTTGGTCGGTCATTCGAACCCCAGAGTCCCGCTCAGAAGAACTCGTCAAGA 4016

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Qy   4458 TCCAGATCATCCTGATCGACAAGACCGGCTTCCATCCGAGTACGTGCTCGCTCGATGCGGA 4517
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Db   3535 CCCGGCACTTCGCCCAATAGCAGCCAGTCCCTTCCCGCTTCAGTGACAACGTCGAGCACA 3476

Qy   4638 CCCGGCACTTCGCCCAATAGCAGCCAGTCCCTTCCCGCTTCAGTGACAACGTCGAGCACA 4697
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Qy   4698 GCTGCGCAAGGAACCGCCCGTCGTCGGCCAGCCACGATAGCCGCGCTGCCTCGTCGTGGAGT 4757
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Qy  3069  AGCAAAAGGCCAGCAAAAGGCCCAGGAACCGTAAAAAGGCCGCCGCTTGCTGGCGTTTTTCCA  3128
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Db  5509  AGCAAAAGGCCAGCAAAAGGCCCAGGAACCGTAAAAAGGCCGCCGCTTGCTGGCGTTTTTCCA  5450

Qy  3129  TAGGCTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAA  3188
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Db  5449  TAGGCTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAA  5390

Qy  3189  CCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCC  3248
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Db  5389  CCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCC  5330

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CDS       2680. .2895
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Qy  3789  ATTATCGTCG                                                    3798
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Qy  3799  -----------------------                                         3799
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Qy  3799  -----------------------                                         3799
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Qy  3901  TAGAACTCCGC----------------GAGGTCGTCCAGCCTCAGCGCCAGCAGCTGAACCAACT  3947
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Qy  3948  CGCGACGGGATCGACGCCCGGGGGTGGGCGAAGAACTCCAGCATGAGACGATCCCCGCTGGAG  4007
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Db  4489  AGGAAGGGCAGCCCGGATGTCAGTGTACTGCCTTCCAGATCAGAGGTGTACTGGTGCATTGAG  4430

Qy  4008  GATCATCATCAGC-----------                                         4018
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DEFINITION	Cloning vector pEC-K18mob2, complete sequence.
ACCESSION	AF445080
VERSION	AF445080.1 GI:17386067
KEYWORDS	.
SOURCE	Cloning vector pEC-K18mob2
ORGANISM	Cloning vector pEC-K18mob2
	other sequences; artificial sequences; vectors.
REFERENCE	1 (bases 1 to 5695)
AUTHORS	Tauch,A., Kirchner,O., Loffler,B., Gotker,S., Puhler,A. and Kalinowski,J.
TITLE	Efficient Electrotransformation of Corynebacterium diphtheriae with a Mini-Replicon Derived from the Corynebacterium glutamicum Plasmid pGA1
JOURNAL	Curr. Microbiol. 45 (5), 362-367 (2002)
PUBMED	12232668
REFERENCE	2 (bases 1 to 5695)
AUTHORS	Tauch,A.
TITLE	Direct Submission
JOURNAL	Submitted (08-NOV-2001) Department of Genetics, University of Bielefeld, Universitaetsstrasse 25, Bielefeld D-33615, Germany
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Qy   4369  TACAAAATCACGGGCGTCGTGGACTATGAGCACGTCCGCCGGAGGCGTCCCGGAAAAACGAT  4310
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Db   4038  TCCGAAGCCCAACCTTCATAGAGACGGCGGTGGAATGAAATCGGTGATGGCAGGTT  4097

Qy   4309  TCCGAAGCCCAACCTTCATAGAGACGGCGGTGGAATGAAATCGGTGATGGCAGGTT  4250
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Qy   4249  GGGCGTCGCTTGGTCGGTCATTCGAACCCGCTCCCGCTCAGAAGAACTCGTCAAGA  4190
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Qy   4457  GGCATGCGCGGCGTTGAGCCTGGCGAACAGTTCGGCTGCGGCGGAGCCCGTCTTCG  4398
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Qy   4637  GCATCAGCCATGATGGATCGACTTTCTCGGCAGGAGCCAAGGTGAGATGACAGGAGATCCTGC  4578
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Db   3769  GCATCAGCCATGATGGATCGACTTTCTCGGCAGGAGCAAGGTGAGATGACAGGAGATCCTGC  3710

Qy   4697  CCCGGCACTTCGCCCAATAGCAGCCAGTCCCTTCCCGCTTCAGTGACAACGTCGAGACA  4638
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Db   3709  CCCGGCACTTCGCCCAATAGCAGCCAGTCCCTTCCCGCTTCAGTGACAACGTCGAGACA  3650

Qy   4757  GCTGCGCAAGGAACGCCCGTCGTGGCCAAGCGCCGTCGGCGCTGCCTGCGTCGTCAGT  4698
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Db   3649  GCTGCGCAAGGAACGCCCGTCGTGGCCAAGCGCCGTCGGCGCTGCCTGCGTCGTTGGAGT  3590

Qy   4817  TCATTCAGGGACCACCGGACAGGTCGTTCTTGACAAAAAGAACCCGGGCGCCCTGCGCTGAC  4758
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Db   3589  TCATTCAGGGACCACCGGACAGGTCGTTCTTGACAAAAAGAACCCGGGCGCCCTGCGCTGAC  3530

Qy   4877  AGCCGGAACACGGCCGCGGCATCAGAGCCGCCAGTTGTCGTGTGCCCAGTCATAGCCGAAT  4818
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Qy   4937  AGCCTCTCCACCAGCGGCCGGAGAACCTGCGTGCAATCCATCTTGTTCAATCATGCGA  4878
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Db   3469  AGCCTCTCCACCAGCGGCCGGAGAACCTGCGTGCAATCCATCTTGTTCAATCATGCGA  3410

Qy   4997  AACGATCCTCATCCTGTCTCTTGATCAGATCTTGATCAGATCCCCTTGGC  4938
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Db   3409  AACGATCCTCATCCTGTCTCTTGATCAGATCTTGATCAGATCCCCTTGGC  3350

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Query Match           39.5%;  Score 2088;  DB 12;  Length 5695;
Best Local Similarity 86.8%;  Pred. No. 0;
  Matches 2433;  Conservative  0;  Mismatches 140;  Indels 231;  Gaps  3;

Qy   2711 CGTAATCATGGTCATAGCTGTTCCTGTGTGTGAAATTGTTATCCGTTCACAATTCCACACA 2770
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Db   5477 CGTAATCATGGTCATAGCTGTTCCTGTGTGTGAAATTGTTATCCGTTCACAATTCCACACA 5418

Qy   2771 ACATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCA 2830
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Db   5417 ACATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCA 5358

Qy   2831 CATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGC 2890
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Db   5357 CATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGC 5298

Qy   2891 ATTAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTT 2950
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Db   5297 ATTAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTT 5238

Qy   2951 CCTCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACT 3010
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Db   5237 CCTCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACT 5178

Qy   3011 CAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAG 3070
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Db   5177 CAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAG 5118

Qy   3071 CAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATA 3130
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Qy   3131 GGCTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACC 3190
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Qy   3191 CGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTG 3250
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Db   4997 CGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTG 4938

Qy   3251 TTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGC 3310
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Db   4757 TTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGA 4698

Qy   3491 TTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACG 3550
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Db   4697 TTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACG 4638

Qy   3551 GCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAA 3610
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Db   4577 AAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTG 4518

Qy   3671 TTTGCAAGCAGCAGATTACGGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGATCTTT 3730
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Qy   3731 CTACGGGGTCTGACGCTCAGTGGAACGAAAACTCACGTTAAGGGATTTTGGTCATGAGAT 3790
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Db   4457 CTACGGGGTCTGACGCTCAGTGGAACGAAAACTCACGTTAAGGGATTTTGGTCATGAGCTT 4398

Qy   3791 TATCGTCG-                                                    3798
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Db   4397 TTCCGCTGCATAACCCTGCTTCGGGGTCATTATAGGCGATTTTTTCGGTATATCCATCCTT 4338

Qy   3799 ----------                                                   3798
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Qy   3799 -------------                                                3799
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Qy   3843 ATGGATGCGCGGATAGCGCGCTGCGTCGTTCCTGGATGCCGACGGGAATCCTGCTGGCC   3902
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Db   4217 CACTGTCCCCTTATTCGCACCTGGCGTGCTCAAGCGGGATAACCTGCTGTTGCCGGCTGGCC 4158

Qy   3903 GAACTCGC---------                                            3949
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Qy   3950 CGAGGGGATCGAGCGCCCGGGCTGGGCGGAAGAACTCCAGCAGATGAGATCCCCGGAGGA 4009
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Qy   4010 TCATCCAGC---------                                           4018
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Qy   4100 GCGTCCGCTTGGTCGGTCATTTCGAACCCCAGAGTCCCGCTCAGAAGAACTCGTCAAGAAG 4159
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DEFINITION   AY222814 Cloning vector pK18mob2, 3035 bp DNA circular SYN 01-OCT-2003
ACCESSION   Cloning vector pK18mob2, complete sequence.
VERSION   AY222814
KEYWORDS   AY222814.1 GI:29242887
SOURCE   .
ORGANISM   Cloning vector pK18mob2
                Cloning vector pK18mob2
                other sequences; artificial sequences; vectors.
REFERENCE   1 (bases 1 to 3035)
AUTHORS   Tauch,A., Zheng,Z., Puhler,A. and Kalinowski,J.
TITLE   Corynebacterium striatum chloramphenicol resistance transposon
                Tn5564: genetic organization and transposition in Corynebacterium
                glutamicum
JOURNAL   Plasmid 40 (2), 126-139 (1998)
MEDLINE   98414982
PUBMED   9735314
REFERENCE   2 (bases 1 to 3035)
AUTHORS   Kirchner,O. and Tauch,A.
TITLE   Tools for genetic engineering in the amino acid-producing bacterium
                Corynebacterium glutamicum
JOURNAL   J. Biotechnol. 104 (1-3), 287-299 (2003)
MEDLINE   22830032
PUBMED   12948646
REFERENCE   3 (bases 1 to 3035)
AUTHORS   Kirchner,O. and Tauch,A.
TITLE   Direct Submission
JOURNAL   Submitted (22-JAN-2003) Department of Genetics, University of
                Bielefeld, Universitaetsstrasse 25, Bielefeld D-33615, Germany
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ORIGIN

Query Match   39.3%; Score 2078; DB 12; Length 3035;
Best Local Similarity 86.7%;   Pred. No. 0;
Matches 2423; Conservative 0; Mismatches 140; Indels 231; Gaps 3;

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Db 3027 GTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCCACACAACATACGAGC 2968

Qy 2781 CGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACATTAATTGC 2840
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Qy 2841 GTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCATTAATGAAT 2900
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Db 2907 GTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCATTAATGAAT 2848

Qy 4220 GTCAGCCCATTCGCCGCCAAGCTCTTCAGCAATATCACGGGTAGCCAACGCTATGTCCTG 4279
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Qy 4640 CGGCACTTCGCCCAATAGCAGCCAGTCCCTTCCCGCTTCAGTGACAACGTCGAGCACAGC 4699
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Qy 5000 CAAGAAAGCCATCCAGTTTACTTTGCAGGGCTTCCCAACCTTACCAGAGGGCGCCCCAGC 5059
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Qy 5060 TGGCAATTCCGGTTCGCTTGCTGTCCATAAAACCGCCCAGTCTAGCTATCGCCATGTAAG 5119
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Db 2837 CCCACTGCAAGCTACCTGCTTTCTCTTTGCGCTTGCGTTTTCCCTTGCGTTTTCCCTTGC 2778

Qy 5180 GTAGTGACATTCATCCGGGGTCAGCACCGTTTCTGCGGACTGGCTTTCTACGTGTTCCG 5239
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Db 2777 GTAGTGACATTCATCCGGGGTCAGCACCGTTTCTGCGGACTGGCTTTCTACGTGTTCCG 2718

Qy 5240 CTTCCTTTAGCAGCCCTTGCGCCCTGAGTGCTTGCGGCAGCGTG 5283
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Db 2717 CTTCCTTTAGCAGCCCTTGCGCCCTGAGTGCTTGCGGCAGCGTG 2674

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Qy  3853 GGATAGCCGCTGCTGGTTTCTGGATGCCGACGATTTGCACTGCCGGTAGAACTCCGC-  3911
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Db  1767 TATTCGCACCTGGCGGTGCTCAACGGGAATCCTGCTCTGCGAGGCTGGCGGCTACCGCC 1708

Qy  3912 ---------GAGGTCGTCCAGGCAGCAGTGAACCAACTCGCGAGGGGGATC         3959
                  |
Db  1707 GGCGTAACAGATGAGGGCAAGCGGATGGCTGATGAAACCAACCAAGCCAACCAGGAGGGCGAGC 1648

Qy  3960 GAGCCCGGGTGGCGGAGAACTCCAGCAGACATGTGAGACAAAAGGCCA-         4018
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Qy  4019 -------------                                             4018
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Qy  4350 TTCGGCAAGCAGGCATCGCCGTCGGGCGATGCGCGCC                        4409
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Db  1167 TTCGGCAAGCAGGCATCGCCGTCGGGCATCCGCGGCC 1108

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Qy  4470 TGATCGACAAGACCGGCCAGTAGCCGCGCCGCAGCCGCCGCATTGCATCAGCCATGG        4529
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Qy  3021 AATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCAAAAGGCCA      3080
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Qy  3681 GCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTC      3740
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ORIGIN

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Qy   2961 TGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCAAAGGCGGT 3020
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SOURCE      Cloning vector pK18PolyF2
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  AUTHORS   Tauch,A., Kirchner,O., Loffler,B., Gotker,S., Puhler,A. and
            Kalinowski,J.
  TITLE     Efficient electrotransformation of Corynebacterium diphtheriae with
            a mini-replicon derived from the Corynebacterium glutamicum plasmid
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  JOURNAL   Curr. Microbiol. 45 (5), 362-367 (2002)
   MEDLINE  22217619
    PUBMED  12232668
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  AUTHORS   Tauch,A., Kirchner,O., Loffler,B., Gotker,S., Puhler,A. and
            Kalinowski,J.
  TITLE     Direct Submission
  JOURNAL   Submitted (22-JAN-2003) Department of Genetics, University of
            Bielefeld, Universitaetsstrasse 25, Bielefeld D-33615, Germany
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Qy 5010 ATCCAGTTTACTTTGCAGGGCTTCCCAACCTTACCAGAGGGCGCCCCAGCTGCAATTCC 5069
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Db 525 ATCCAGTTTACTTTGCAGGGCTTCCCAACCTTACCAGAGGGCGCCCCAGCTGCAATTCC 466

Qy 5070 GGTTCGCTTGCTGTCATAAAACCGCCCAGTCTAGCTATCGCCATGTAAGCCCACTGCAA 5129
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 465 GGTTCGCTTGCTGTCATAAAACCGCCCAGTCTAGCTATCGCCATGTAAGCCCACTGCAA 406

Qy 5130 GCTACCTGCTTCTCTTTGCGCTTGCGTTTTCCCTTGTCCCAGATAGTCCAGTAGCTGACA 5189
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 405 GCTACCTGCTTCTCTTTGCGCTTGCGTTTTCCCTTGTCCCAGATAGTCCAGTAGCTGACA 346

Qy 5190 TTCATCCGGGGTCAGCACCGTTTCTGCGGACTGGCTTTCTACGTGTTCCTTTAG 5249
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db 345 TTCATCCGGGGTCAGCACCGTTTCTGCGGACTGGCTTTCTACGTGTTCCTTTAG 286

Qy 5250 CAGCCCCTTGCGCCCTGAGTGCTTGCGGCAGCGTG 5283
          |||||||||||||||||||||||||||||||
Db 285 CAGCCCCTTGCGCCCTGAGTGCTTGCGGCAGCGTG 252

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OM nucleic - nucleic search, using sw model

GenCore version 5.1.6
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Run on: July 3, 2005, 01:00:02 ; Search time 2542 Seconds
(without alignments)
12302.909 Million cell updates/sec

Title: US-09-921-143-36
Perfect score: 5283
Sequence: 5283
1 aagcttgaccttatgcgact.........tgagtgcttgcggcagcgtg 5283

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 439O206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_16Dec04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		5283	100.0	5283	6	ABK10062	Abk10062 Expressio
2		2240	42.4	8349	3	AAA15565	Aaa15565 pMON30464
3	c	2017.2	38.2	6136	2	AAV29673	Aav29673 Hybrid NA
4	c	1793.4	33.9	4800	2	AAX52020	Aax52020 Synthetic
5	c	1652.4	31.3	5594	2	AAV33629	Aav33629 GENSA 981
6	c	1634.4	30.9	4245	12	ADJ71288	Adj71288 PCR-Blunt
7	c	1634.4	30.9	5285	4	AAH74865	Aah74865 Nucleotid
8	c	1634.4	30.9	6233	13	ADS75100	Ads75100 Plasmid p
9	c	1632.8	30.9	5285	8	ABX94355	Abx94355 Rolling c
10	c	1618.2	30.6	6561	2	AAV33630	Aav33630 Plasmid V
11		1603.8	30.4	2192	6	ABQ78294	Abq78294 Nucleotid
12		1603.8	30.4	3534	6	ABQ78293	Abq78293 Nucleotid
13		1603.8	30.4	3534	9	AAL62060	Aal62060 TV-GRHH p
14		1603.8	30.4	3534	9	AAL62062	Aal62062 Wild-type
15		1603.8	30.4	3534	9	AAL62059	Aal62059 TI-GRHH p
16		1603.8	30.4	3534	9	AAL62058	Aal62058 pSP-HV-GH
17		1603.8	30.4	3534	9	AAL62061	Aal62061 15/27/28-
18		1603.8	30.4	3534	9	AAL60444	Aal60444 TI-GRHH p
19		1603.8	30.4	3534	9	AAL60445	Aal60445 TV-GRHH p
20		1603.8	30.4	3534	9	AAL60446	Aal60446 15/27/28
21		1603.8	30.4	3534	9	AAL60443	Aal60443 pSP-HV-GH
22		1603.8	30.4	3534	9	AAL60447	Aal60447 Wild-type
23		1603.8	30.4	3534	10	ACF04661	Acf04661 Wildtype
24		1603.8	30.4	3534	10	ACF04660	Acf04660 15/27/28
25		1603.8	30.4	3534	10	ACF04657	Acf04657 HV-GRHH o
26		1603.8	30.4	3534	10	ACF04659	Acf04659 TV-GRHH o
27		1603.8	30.4	3534	10	ACF04658	Acf04658 TI-GRHH o
28		1603.8	30.4	3534	12	ADF90306	Adf90306 Wild type
29		1603.8	30.4	3534	12	ADF90302	Adf90302 HV-GRHH p
30		1603.8	30.4	3534	12	ADF90304	Adf90304 TV-GRHH p
31		1603.8	30.4	3534	12	ADF90305	Adf90305 15/27/28
32		1603.8	30.4	3534	12	ADF90303	Adf90303 TI-GRHH p
33		1603.8	30.4	3534	12	ADL70452	Adl70452 Protease
34		1603.8	30.4	3534	12	ADL70453	Adl70453 Protease
35		1603.8	30.4	3534	12	ADL70454	Adl70454 Protease
36		1603.8	30.4	3534	12	ADO31099	Ado31099 Cardiac s
37		1603.8	30.4	3534	12	ADO31100	Ado31100 Cardiac s
38		1603.8	30.4	3534	12	ADO31098	Ado31098 Cardiac s
39		1603.8	30.4	3534	12	ADO31101	Ado31101 Cardiac s
40		1603.8	30.4	3534	13	ADR23409	Adr23409 Codon opt
41		1603.8	30.4	3534	13	ADR23393	Adr23393 TI-GRHH p
42		1603.8	30.4	3534	13	ADR23394	Adr23394 TV-GRHH p
43		1603.8	30.4	3534	13	ADR23395	Adr23395 15/27/28
44		1603.8	30.4	3534	13	ADR23392	Adr23392 Plasmid p
45		1603.8	30.4	3534	13	ADR23396	Adr23396 Plasmid e

ALIGNMENTS

RESULT 1
ABK10062
ID   ABK10062 standard; DNA; 5283 BP.
XX
AC   ABK10062;
XX
DT   21-MAY-2002 (first entry)
XX
DE   Expression vector construct pVGI.1 containing VEGF-2 insert.
XX
KW   Human; vascular endothelial growth factor 2; VEGF-2; ds; pVGI.1;
KW   chronic limb ischaemia; myocardial ischaemia; autoimmune disorder; pHE4a;
KW   allergic reaction; organ rejection; inflammatory condition; arrhythmia;
KW   hyperproliferative disorder; viral infection; bacterial infection;
KW   fungal infection; parasitic infection; cardiovascular disorder; embolism;
KW   heart valve disease; aneurysm; arterial occlusive disorder; gene therapy.
XX
OS   Synthetic.
XX
PN   WO20021176S-A1.
XX
PD   14-FEB-2002.
XX
PF   03-AUG-2001; 2001WO-US024658.
XX
PR   04-AUG-2000; 2000US-0223276P.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Coleman TA;
XX
DR   WPI; 2002-217153/27.
XX
PT   Isolated nucleic acid having expression vector construct with vascular
PT   endothelial growth factor-2 insert, useful for treating chronic limb
PT   ischaemia or myocardial ischaemia, autoimmune disorders and allergic
PT   conditions.
XX
PS   Disclosure; Fig 31; 241pp; English.
XX
CC   The invention relates to an isolated nucleic acid comprising pVGI.1
CC   expression vector construct containing the vascular endothelial growth
CC   factor 2 (VEGF-2) insert. The nucleic acid is useful for producing a host

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CC  cell by transducing, transforming or transfecting a host cell with the
CC  DNA and for treating a patient having chronic limb ischaemia or
CC  myocardial ischaemia, or a disease or disorder selected from autoimmune
CC  disorders (e.g. rheumatoid arthritis, dermatitis), allergic reactions or
CC  conditions (e.g. asthma), organ rejection, inflammatory conditions (e.g.
CC  Crohn's disease), hyperproliferative disorders (e.g. Gaucher's disease),
CC  diseases due to viral, bacterial, fungal or parasitic infection,
CC  cardiovascular disorders (e.g. cardiomyopathy), arrhythmia, heart valve
CC  diseases, aneurysms, arterial occlusive disorders and embolism. This
CC  sequence represents the pVGI.1 expression vector containing the VEGF-2
CC  insert
XX
SQ  Sequence 5283 BP; 1244 A; 1422 C; 1417 G; 1200 T; 0 U; 0 Other;

Query Match    100.0%;  Score 5283;  DB 6;  Length 5283;
Best Local Similarity  100.0%;  Pred No. 0;
Matches 5283;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;
```

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Qy          1 AAGCTTGACCTTATGCGACTTCCTACTTGGCAGTACATCTACGTATTAGTCATCGCTAT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AAGCTTGACCTTATGCGACTTCCTACTTGGCAGTACATCTACGTATTAGTCATCGCTAT 60

Qy         61 TACCATGGTGTGATGCGGTTTTGGCAGTACATCAATGGGCGTGGATACGCGGTTTGACTCACG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TACCATGGTGTGATGCGGTTTTGGCAGTACATCAATGGGCGTGGATACGCGGTTTGACTCACG 120

Qy        121 GGGATTTCCAAGTCTTCCACCCCACTGACGTCAATGGGAGTTTGTTTTGGCACCAAAATCA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGGATTTCCAAGTCTTCCACCCCACTGACGTCAATGGGAGTTTGTTTTGGCACCAAAATCA 180

Qy        181 ACGAGACTTTCCAAAATGTCTAACAACTCCGCCCCATTGACGCAAATGGGCGGTAGGGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACGAGACTTTCCAAAATGTCTAACAACTCCGCCCCATTGACGCAAATGGGCGGTAGGGC 240

Qy        241 AACAATGCTTATGAGTTAACGGTGAGTTAGCAACATGCCTTATAAGGAGAGAACAAAGACCGTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AACAATGCTTATGAGTTAACGGTGAGTTAGCAACATGCCTTATAAGGAGAGAACAAAGACCGTG 300

Qy        301 CATGGCCGATTGGTGGGAGTAAGGTGTATGATCGTGGTATCGTGCCTTGTTGGGGAGGAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CATGGCCGATTGGTGGGAGTAAGGTGTATGATCGTGGTATCGTGCCTTGTTGGGGAGGAG 360

Qy        361 GCAACAGACGGGTCTAACACGGATTGGACGAACCACTGAATTCCCGATTCCGCAGAGATATT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCAACAGACGGGTCTAACACGGATTGGACGAACCACTGAATTCCCGATTCCGCAGAGATATT 420

Qy        421 GTATTTAAGTGCCCCAGCTCGATACAATAAACGCCATTGACCATTCACCACATTGGTGTG 480
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GTATTTAAGTGCCCCAGCTCGATACAATAAACGCCATTGACCATTCACCACATTGGTGTG 480

Qy        481 CACCTGGGTTGGGATCGATCCATCATGCACTCGCTGGGCTTCTCTCGTGGCGTGTTCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CACCTGGGTTGGGATCGATCCATCATGCACTCGCTGGGCTTCTCTCGTGGCGTGTTCT 540

Qy        541 CTGCTCGCGCCGCTGCGCTTCCTCGCCGGTCCTCGCGAGGCGCCCGCGCCGCCGGCCGCCTTC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CTGCTCGCGCCGCTGCGCTTCCTCGCCGGTCCTCGCGAGGCGCCCGCGCCGCCGGCCGCCTTC 600

Qy        601 GAGTCCGACTCGACCTCTCGACCGCGAGCGGGTGAGGCCCACGCGGCTTATGCA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GAGTCCGACTCGACCTCTCGACCGCGAGCGGGTGAGGCCCACGCGGCTTATGCA 660

Qy        661 AGCAAAGATCGGAGAGACAGCAGTTACGGTCTGTGTCCAGTGAGTTAACTCATGACTGTA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AGCAAAGATCGGAGAGACAGCAGTTACGGTCTGTGTCCAGTGAGTTAACTCATGACTGTA 720

Qy        721 CTCTACCCAGAATATTGGAAAAATGTACAAGGTCAGCTAAGGAAAGGAGAGGGCTGGCAACAT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CTCTACCCAGAATATTGGAAAAATGTACAAGGTCAGCTAAGGAAAGGAGAGGGCTGGCAACAT 780

Qy        781 AACAGAGAACAGGCCAACCTCAACTCAAGGACAGAAGAGACTATAAAATTTGCTGCAGCA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACAGAGAACAGGCCAACCTCAACTCAAGGACAGAAGAGACTATAAAATTTGCTGCAGCA 840

Qy        841 CATTATAATACAGAGATCTTGAAAAGTATTGATAATGAGTGGAGAAAGACTCAATGCATG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CATTATAATACAGAGATCTTGAAAAGTATTGATAATGAGTGGAGAAAGACTCAATGCATG 900

Qy        901 CCACGGGAGGTGTGTATAGATGTGGGAAGGAGTTGGAGTCGGCAGAACACCTTCTTT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 CCACGGGAGGTGTGTATAGATGTGGGAAGGAGTTGGAGTCGGCAGAAACACCTTCTTT 960

Qy        961 AAACCCCATGTGTCCGTCTACAGATGTGGGGGTGCTGCAATGTGAGGGGCGTGCAG 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AAACCCCATGTGTCCGTCTACAGATGTGGGGGTGCTGCAATGTGAGGGGCGTGCAG 1020

Qy       1021 TGCATGAACACCAGCACGAGCTACCTCAGCAAGACGTTATTGAAATTACACTGCCTCTC 1080
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 TGCATGAACACCAGCACGAGCTACCTCAGCAAGACGTTATTGAAATTACACTGCCTCTC 1080

Qy       1081 TCTCAAGGCCCCAAACCAGTAACAATCAGTTTGCCAATCACACTTCCTGCCGATGCATG 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 TCTCAAGGCCCCAAACCAGTAACAATCAGTTTGCCAATCACACTTCCTGCCGATGCATG 1140

Qy       1141 TCTAAACTGGATGTTTACAGACAAGTTCATTCCATTATTAGACGTTCCCTGCCAGCAACA 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TCTAAACTGGATGTTTACAGACAAGTTCATTCCATTATTAGACGTTCCCTGCCAGCAACA 1200

Qy       1201 CTACCAGTGTCAGGCAGCAGCGAACAAGACCTGCCCCACCAATTACATGTGGAATAATCAC 1260
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Db       1201 CTACCAGTGTCAGGCAGCAGCGAACAAGACCTGCCCCACCAATTACATGTGGAATAATCAC 1260

Qy       1261 ATCTGCAGATGCCTGGCTCAGGAAGATTTTATGTTTTCCTCGGATGCTGGAGATGACTCA 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 ATCTGCAGATGCCTGGCTCAGGAAGATTTTATGTTTTCCTCGGATGCTGGAGATGACTCA 1320

Qy       1321 ACAGATGGATTCCATGACACATCTGTGACCAACAAGGAGCTGGATGAAGAAGACCTGTCAG 1380
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 ACAGATGGATTCCATGACACATCTGTGACCAACAAGGAGCTGGATGAAGAAGACCTGTCAG 1380

Qy       1381 TGTGTCTGCAGAGCGGGCCTTCGCGCCGCTGGGACCCCAGCTGTGGGACCCAACAGA 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 TGTGTCTGCAGAGCGGGCCTTCGCGCCGCTGGGACCCCAGCTGTGGGACCCAACAGA 1440

Qy       1441 AACTCATGCCAGTGTCTGTAAAAACAAACTCTTCCCAGCCAATGTGGGGCCAACCGA 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 AACTCATGCCAGTGTCTGTAAAAACAAACTCTTCCCAGCCAATGTGGGGCCAACCGA 1500

Qy       1501 GAATTTGATGAAAACACATGCCAGTGTGTATGTAAAAGAACTCACATTGTGTG 1560
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 GAATTTGATGAAAACACATGCCAGTGTGTATGTAAAAGAACTCACATTGTGTG 1560

Qy       1561 CTAAATCCTGGAAAATGTGCCTGTGAATGTACAGAAGTCCTACCCTGTACCCGGCTTTGTTAAAA 1620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 CTAAATCCTGGAAAATGTGCCTGTGAATGTACAGAAGTCCTACCCTGTACCCGGCTTTGTTAAAA 1620

Qy       1621 GGAAAGAAGTTCCACCACCAAAACATCGAGCTGTTACGAGACGGCCATGTACGAACCGCCAG 1680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 GGAAAGAAGTTCCACCACCAAAACATCGAGCTGTTACGAGACGGCCATGTACGAACCGCCAG 1680

Qy       1681 AAGGCTTGTGAGCCAGGATTTTCATATAGTGAAGAAGTGTGTCGTTGTGTCCCTTCATAT 1740
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Db       1681 AAGGCTTGTGAGCCAGGATTTTCATATAGTGAAGAAGTGTGTCGTTGTGTCCCTTCATAT 1740

Qy       1741 TGGAAAAGACCACCAAATGAGCTAATCTAGAATCCGTACCCTGCCAGGCTTTTGTCAAAC 1800
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1741 TGGAAAAGACCACCAAATGAGCTAATCTAGAATCCGTACCCTGCCAGGCTTTTGTCAAAC 1800

Qy       1801 AGCACCTTTGTTGGTTCCACTTGGTGGAGCTCTCTACCTGGTGTGTGGGGAGCGTGGAT 1860
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Db       1801 AGCACCTTTGTTGGTTCCACTTGGTGGAGCTCTCTACCTGGTGTGTGGGGAGCGTGGAT 1860

Qy       1861 TCTTCTACACACCCCATGTGCCCGCCGCCAAGTGGAGGACCCCAAGTGGAGCTCTGCTCCT 1920
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1861 TCTTCTACACACCCCATGTGCCCGCCGCCAAGTGGAGGACCCCAAGTGGAGCTCTGCTCCT 1920
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Qy  1921 GAATTCTATCCCAAGTGCTCTAACTACCCTGTTTGTCTTTCACCCTTGAGACCTTGTAAATT 1980
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Db  1921 GAATTCTATCCCAAGTGCTCTAACTACCCTGTTTGTCTTTCACCCTTGAGACCTTGTAAATT 1980

Qy  1981 GTGCCCTAGGTGTGGAGGGTCTCAGGCTAACCAGTGGGGGCACATTCTGTTGGGCAGCT 2040
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1981 GTGCCCTAGGTGTGGAGGGTCTCAGGCTAACCAGTGGGGGCACATTTCTGTTGTGGGCAGCT 2040

Qy  2041 AGACATATGTAAACATGTAGCTGCCAGGAAGAGTGAGAATCCTTCCTTAAGTCTCCTA 2100
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2041 AGACATATGTAAACATGTAGCTGCCAGGAAGAGTGAGAATCCTTCCTTAAGTCTCCTA 2100

Qy  2101 GGTGGTGACGGGTGGCTAGGCCCCAGGATAGGTACCTATTTGGGGACCCCATAGAGCACT 2160
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Db  2101 GGTGGTGACGGGTGGCTAGGCCCCAGGATAGGTACCTATTTGGGGACCCCATAGAGCACT 2160

Qy  2161 GCACTGACTGAGGGATGGTAACAGGTGTAACAGGATGTGTAGGTTTTGGAGGCCCATATGTCCATTCAT 2220
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2161 GCACTGACTGAGGGATGGTAACAGGTGTAACAGGATGTGTAGGTTTTGGAGGCCCATATGTCCATTCAT 2220

Qy  2221 GACCAGTGACTTGTCTCACAGCGTCATGCAACCCTTGCCTCCTGTGCTTAGCAGGGGA 2280
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2221 GACCAGTGACTTGTCTCACAGCGTCATGCAACCCTTGCCTCCTGTGCTTAGCAGGGGA 2280

Qy  2281 TAAAGTGAGAGAAAGCCTGGCTAATCAGGGGGTCGCTCAGCTCCTCCTAACTGGATTGT 2340
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2281 TAAAGTGAGAGAAAGCCTGGCTAATCAGGGGGTCGCTCAGCTCCTCCTAACTGGATTGT 2340

Qy  2341 CCTATGTGTCTTGCTTCTGTGCTTGATGCTCTGCCCTGTGCTGACATGACCTCCCTG 2400
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2341 CCTATGTGTCTTGCTTCTGTGCTTGATGCTCTGCCCTGTGCTGACATGACCTCCCTG 2400

Qy  2401 GCAGTGCACACTGGAGCTGGAGGCCCGGGGGCAGGTGACCTTCAGACCTTGGCA 2460
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2401 GCAGTGCACACTGGAGCTGGAGGCCCGGGGGCAGGTGACCTTCAGACCTTGGCA 2460

Qy  2461 CTGGAGGTGGCCCGGAGCAGCCGGAAGCGCGGCCATCGTGGATCAGTGCTCGCACCAGCATCTGCTCT 2520
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2461 CTGGAGGTGGCCCGGAGCAGCCGGAAGCGCGGCCATCGTGGATCAGTGCTCGCACCAGCATCTGCTCT 2520

Qy  2521 CTCTACCAACTGCGAGAACTACTGCACTACTAGGCCCACCACTACCCTGCTCCACCCCTCTGCA 2580
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Db  2521 CTCTACCAACTGCGAGAACTACTGCACTACTAGGCCCACCACTACCCTGCTCCACCCCTCTGCA 2580

Qy  2581 ATGAATAAAACCTTTGAAAGAGCACTACAAGTGTGTGTACAAGCGGTGCATGTGCATATG 2640
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2581 ATGAATAAAACCTTTGAAAGAGCACTACAAGTGTGTGTACAAGCGGTGCATGTGCATATG 2640

Qy  2641 TGGTGCGGGGAACATGAGTGGGGGCTGGCCTGGGAGCTTAATCTATCTGGCA 2700
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2641 TGGTGCGGGGGAACATGAGTGGGGGCTGGCCTGGGAGCTTAATCTATCTGGCA 2700

Qy  2701 GCTGTCAGCTGAACGTAATCATGGTCATAGCTCATTGTTTCCTGTGTGAAATTGTTATCCGCTCACA 2760
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2701 GCTGTCAGCTGAACGTAATCATGGTCATAGCTCATTGTTTCCTGTGTGAAATTGTTATCCGCTCACA 2760

Qy  2761 ATTCCACACAACATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTG 2820
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2761 ATTCCACACAACATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTG 2820

Qy  2821 AGCTAACTCACATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCG 2880
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2821 AGCTAACTCACATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCG 2880

Qy  2881 TGCCAGCTGCATTAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGC 2940
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2881 TGCCAGCTGCATTAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGC 2940

Qy  2941 TCTTCCGCTTCCTCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTA 3000
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2941 TCTTCCGCTTCCTCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTA 3000

Qy  3001 TCAGCTCACTCAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAG 3060
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3001 TCAGCTCACTCAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAG 3060

Qy  3061 AACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCG 3120
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3061 AACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCG 3120

Qy  3121 TTTTTCCATAGGCTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGG 3180
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3121 TTTTTCCATAGGCTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGG 3180

Qy  3181 TGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTG 3240
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3181 TGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTG 3240

Qy  3241 CGCTCCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGA 3300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3241 CGCTCCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGA 3300

Qy  3301 AGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGC 3360
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3301 AGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGC 3360

Qy  3361 TCCAAGCTGGGCTGTGTGCACGAACCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGT 3420
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3361 TCCAAGCTGGGCTGTGTGCACGAACCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGT 3420

Qy  3421 AACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACT 3480
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3421 AACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACT 3480

Qy  3481 GGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGG 3540
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3481 GGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGG 3540

Qy  3541 CCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTT 3600
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3541 CCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTT 3600

Qy  3601 ACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGT 3660
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3601 ACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGT 3660

Qy  3661 GGTTTTTTTGTTTGCAAGCAGCAGATTACGGCGCAGAAAAAAAGGATCTCAAGAAGATCCT 3720
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3661 GGTTTTTTTGTTTGCAAGCAGCAGATTACGGCGCAGAAAAAAAGGATCTCAAGAAGATCCT 3720

Qy  3721 TTGATCTTTTCTACGGGTCTGACGCTCAGTGGAACGAAAACTCACGTTAAGGGATTTTTG 3780
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3721 TTGATCTTTTCTACGGGTCTGACGCTCAGTGGAACGAAAACTCACGTTAAGGGATTTTTG 3780

Qy  3781 GTCATGAGATTATCGTCGCCAAAGCTGGCCATCGTGCTCCACTCCTGCGAGTTCGGGG 3840
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3781 GTCATGAGATTATCGTCGCCAAAGCTGGCCATCGTGCTCCACTCGTGCGAGTTCGGGG 3840

Qy  3841 GCATGATGCCGCGGATAGCCCGTGCTGGTTTCCTGATGCCGCCGGATTTGCACTGCGCGG 3900
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3841 GCATGATGCCGCGGATAGCCCGTGCTGGTTTCCTGATGCCGCCGGATTTGCACTGCGCGG 3900

Qy  3901 TAGAACTCCGCGAGGTGGGGAAGAACTCAGCATGAGCAGCTGCGACCAACTCGACGGGATCG 3960
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3901 TAGAACTCCGCGAGGTGGGGAAGAACTCAGCATGAGCAGCTGCGACCAACTCGACGGGATCG 3960

Qy  3961 AGCCCGGGGTGGGGAAGAACTCAGCATGAGATCATCCGCGCGCTGGAGGATCATCCAGCCG 4020
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3961 AGCCCGGGGTGGGGAAGAACTCAGCATGAGATCATCCGCGCGCTGGAGGATCATCCAGCCG 4020

Qy  4021 GCGTCCCGGAAAACGATTCCGAAGCCCAACCTTTCATAGAAGGCGGCGGTGGAATCGAAA 4080
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4021 GCGTCCCGGAAAACGATTCCGAAGCCCAACCTTTCATAGAAGGCGGCGGTGGAATCGAAA 4080

Qy  4081 TCTCGTGATGGCAGGTTGGGCGTCGCTTGGTCGGTCATTTCGAACCCCAGAGTCCCGCTC 4140
```

Db 4081 TCTCGTGATGCAGGTTGGGCGTCGCTTGGTCGGTCATTTCGAACCCCAGAGTCCCGCTC 4140

Qy 4141 AGAAGAACTCGTCAAGAGGAAGGCGATAGAAGGCGATGCGCTGCGAATCGGCAGCGGCGGCGATAC 4200
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4141 AGAAGAACTCGTCAAGAGGAAGGCGATAGAAGGCGATGCGCTGCGAATCGGCAGCGGCGGCGATAC 4200

Qy 4201 CGTAAAGCACAGAGGAAGGCGGTCAGCCCATTCGCCGCCAAGCTCTTCGCAGCAATATCACGGG 4260
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4201 CGTAAAGCACAGAGGAAGGCGGTCAGCCCATTCGCCGCCAAGCTCTTCGCAGCAATATCACGGG 4260

Qy 4261 TAGCCAACGTCATGTCCTGATAGCGGTCCGCCACACCCAGCCGCCACAGTCGATGAATC 4320
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4261 TAGCCAACGTCATGTCCTGATAGCGGTCCGCCACACCCAGCCGCCACAGTCGATGAATC 4320

Qy 4321 CAGAAAAGCGGCCATTTCCACCATGATATTCGGCAAGCAGGCATCGCCATGGGTCACGA 4380
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4321 CAGAAAAGCGGCCATTTCCACCATGATATTCGGCAAGCAGGCATCGCCATGGGTCACGA 4380

Qy 4381 CGAGATCCTCCGCGTCGGGCATGCGCGCCTTGAGCCTGGCCGAACAGTTCGGCTGCGCGGA 4440
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4381 CGAGATCCTCCGCGTCGGGCATGCGCGCCTTGAGCCTGGCCGAACAGTTCGGCTGCGCGGA 4440

Qy 4441 GCCCCTGATGCTCTTCGTCCAGATCATCCTGATCGACAAGACCGGCTTCCATCCGAGTAC 4500
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4441 GCCCCTGATGCTCTTCGTCCAGATCATCCTGATCGACAAGACCGGCTTCCATCCGAGTAC 4500

Qy 4501 GTGCTCGCTGCTGATGGCGATGTTTCGCTTGGTGGTCGAATGGGCAGTGGCGGATCAAGCG 4560
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4501 GTGCTCGCTGCTGATGGCGATGTTTCGCTTGGTGGTCGAATGGGCAGTGGCGGATCAAGCG 4560

Qy 4561 TATGCAGCCGCCGCATTCGATCAGCCATGATGCATGATACTTTCTCGGCAAGGTGAG 4620
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4561 TATGCAGCCGCCGCATTCGATCAGCCATGATGCATGATACTTTCTCGGCAAGGTGAG 4620

Qy 4621 ATGACAGGAGATCCTGCCCCGGCACTTCGCCCGGCCCAATAGCAGCCAGTCCCTTCCGCTTCAG 4680
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4621 ATGACAGGAGATCCTGCCCCGGCACTTCGCCCGGCCCAATAGCAGCCAGTCCCTTCCGCTTCAG 4680

Qy 4681 TGACAACGTCGAGCACAGCTGCGCAAGGAACGCCCGTCGTGGCCAGCCACGATAGCCGCG 4740
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4681 TGACAACGTCGAGCACAGCTGCGCAAGGAACGCCCGTCGTGGCCAGCCACGATAGCCGCG 4740

Qy 4741 CTGCCTCGTCCTCTGCAGTTCATTCAGGGCACCGGACAGGTCGGTCTTGACAAAAAGAACCG 4800
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4741 CTGCCTCGTCCTCTGCAGTTCATTCAGGGCACCGGACAGGTCGGTCTTGACAAAAAGAACCG 4800

Qy 4801 GGGCGCCCTGCGCTGACAGCCGGAACACGGGCATCAGACGGCAGCCGATTGTCTGTTGTG 4860
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4801 GGGCGCCCTGCGCTGACAGCCGGAACACGGGCATCAGACGGCAGCCGATTGTCTGTTGTG 4860

Qy 4861 CCCAGTCATAGCCGAATAGCCTCTCCACCCAAGCGGCCGGAGAACCTGCGTGCAATCCAT 4920
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4861 CCCAGTCATAGCCGAATAGCCTCTCCACCCAAGCGGCCGGAGAACCTGCGTGCAATCCAT 4920

Qy 4921 CTTGTTCAATCATGCCGAAACATCCTCTTCTTGATCGGATCTTGATCCCCTGC 4980
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4921 CTTGTTCAATCATGCCGAAACATCCTCTTCTTGATCGGATCTTGATCCCCTGC 4980

Qy 4981 GCCATCAGATCCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTGCAGGGCTTCCCAACCT 5040
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4981 GCCATCAGATCCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTGCAGGGCTTCCCAACCT 5040

Qy 5041 TACCCAGGGGCGCCCATGTAAGCCACTGCAAGCTACCTGCTTTCTCTTTGCGCTTGGTTTT 5100
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 5041 TACCCAGGGGCGCCCCAGCTGGCAATTCCGGTTCGCTTGCTGTCCATAAAACCGCCCAGT 5100

Qy 5101 CTAGCTATCGCCAATGTAAGCCCACTGCAAGCTACCTGCTTTCTCTTTGCGCTTGGTTTT 5160
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 5101 CTAGCTATCGCCAATGTAAGCCCACTGCAAGCTACCTGCTTTCTCTTTGCGCTTGGTTTT 5160

Qy 5161 CCCTTGTCCAGATAGCCCAGTAGCTGACATTCATCCGGGGTCAGCACCGTTTCTGCGGAC 5220
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 5161 CCCTTGTCCAGATAGCCCAGTAGCTGACATTCATCCGGGGTCAGCACCGTTTCTGCGGAC 5220

Qy 5221 TGGCTTTCTACGTGTTCCGCTTCCTTTAGCAGCCCTTGCGCCCTGAGTGCTTGCGGCAGC 5280
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 5221 TGGCTTTCTACGTGTTCCGCTTCCTTTAGCAGCCCTTGCGCCCTGAGTGCTTGCGGCAGC 5280

Qy 5281 GTG 5283
         |||
Db 5281 GTG 5283

RESULT 2
AAA15565
ID   AAA15565   standard; DNA; 8349 BP.
XX
AC   AAA15565;
XX
DT   28-JUL-2000   (first entry)
XX
DE   pMON30464 plasmid.
XX
KW   Transgenic plant; insect resistance; cry2Aa delta-endotoxin; Coleopteran;
KW   Lepidopteran; Dipteran; plastid transit peptide; zmSSU PTP; insecticidal;
KW   plastid targeting peptide; pMON30464 plasmid; expression vector; ds.
OS   Synthetic.
XX
PN   WO200026371-A1.
XX
PD   11-MAY-2000.
XX
PF   04-NOV-1999;   99WO-US026086.
XX
PR   04-NOV-1998;   98US-00186002.
XX
PA   (MONS) MONSANTO CO.
XX
PI   Corbin DR, Romano CP;
XX
DR   WPI; 2000-376130/32.
XX
PT   New method of expressing insecticidal proteins in plants transformed with
PT   a Bacillus thuringiensis delta-endotoxin encoding gene resulting in
PT   effective control of susceptible target pests.
XX
PS   Example 1; Page 96-99; 104pp; English.
XX
CC   Bacillus thuringiensis produce delta-endotoxins during sporulation. These
CC   proteins are toxic to certain insects e.g. Lepidopteran and Coleopteran
CC   larvae. An insect-resistant transgenic plant has been constructed which
CC   contains the delta-endotoxin cry2Ab gene. The present sequence would be
CC   used to transfer delta-endotoxin genes into plant cells and for
CC   subsequent high expression of the cry2Ab gene. Protection may be attained
CC   against insects such as Ostrina spp., Diatraea spp., Helicoverpa spp.,
CC   and Spodoptera spp., in Zea mays; Heliothis virescens, Helicovera spp.,
CC   Pectinophora spp., in Gossypium hirsutum; Anticarsi spp., Pseudoplusia
CC   spp., Epinotia spp., in Glycine max; and Scirpophaga incertulas in Oryza
CC   sativa. Expression of the endotoxin by a plant cell produces a fusion
CC   protein comprising an amino-terminal plastid transit peptide (zmSSU PTP)
CC   covalently linked to the delta-endotoxin. The fusion protein functions to
CC   localise the delta-endotoxin to a subcellular organelle or compartment
XX
SQ   Sequence 8349 BP; 1959 A; 2355 C; 2088 G; 1947 T; 0 U; 0 Other;

Query Match   42.4%;   Score 2240;   DB 3;   Length 8349;
Best Local Similarity   93.4%;   Pred. No. 0;
Matches 2409;   Conservative   0;   Mismatches   25;   Indels   144;   Gaps   1;

Qy 2706 CTAGACGTAATCATGTCATAGCTGTTTCCTGTGTGTGAAATTGTTATCCGCTTCACAATTCC 2765
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 5911 CTTGGGTAATCATCATGTCATAGCTGTTTCCTGTGTGTGAAATTGTTATCCGCTTCACAATTCC 5970

Qy 2766 ACACAACATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTA 2825
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 5161

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Qy   4986  CAGATCCTTGGCGGCCAAGAAAGCCATCCAGTTACTTGCAGGGCGCTCCCAACCTTACCA  5045
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   8047  CAGATCCTTGCGGCGCCAAGAAAAGCCATCCAGTTACTTGCAGGGCGCTCCCAACCTTACCA  8106

Qy   5046  GAGGGCGCCCCAGCTGGCAATTCCGGTTCGCTTGCTTGCGTTGCTTGCTGTCCATAAAACCGCCCAGTCTAGC  5105
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   8107  GAGGGGCGCCCCAGCTGGCAATTCCGGTTCGCTTGCTTGCGTTGCTTGCTGTCCATAAAACCGCCCAGTCTAGC  8166

Qy   5106  TATCGGCCATGTAAGGCCACTGCAAGCTACCTGCTTCTCTTTGCGTTGCGTTTTCCCTT  5165
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   8167  TATCGGCCATGTAAGGCCACTGCAAGCTACCTGCTTCTCTTTGCGTTTCTCTTTCCCTT  8226

Qy   5166  GTCCAGATAGCCCAGTAGCTGACATTCATCCGGGGTCAGCACCCGTTTCTGCGGACTGGCT  5225
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   8227  GTCCAGATAGCCCAGTAGCTGACATTCATCCGGGGTCAGCACCCGTTTCTGCGGACTGGCT  8286

Qy   5226  TTCTACGTGTTCCGCTTCCTTTAGCAGCCCCTGCGCCCTGAGTGCTTGCGGCAGCGTG  5283
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   8287  TTCTACGTGTTCCGCTTCCTTTAGCAGCCCCTGCGCCCTGAGTGCTTGCGGCAGCGTG  8344
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RESULT 3
AAV29673/c
ID AAV29673   standard; cDNA; 6136 BP.
XX
AC AAV29673;
XX
DT 01-SEP-1998 (first entry)
XX
DE Hybrid NAMK.6 (termamyl-linker-CBDEGV) nucleotide sequence.
XX
KW Starch; liquefaction; sweetener; enzyme hybrid; endoglucanase; enzyme;
KW cellulose binding domain; CBD; starch processing; alpha-amylase;
KW saccharification; Termamyl-linker-CBD fusion; ss.
XX
OS Bacillus sp.
OS Humicola insolens.
XX
PN WO9816633-A1.
XX
PD 23-APR-1998.
XX
PF 13-OCT-1997; 97WO-DK000448.
XX
PR 11-OCT-1996; 96DK-00001130.
XX
PA (NOVO) NOVO-NORDISK AS.
XX
PI Bjornvad M, Pedersen S, Schulein M, Bisgardfrantzen H;
XX
DR WPI; 1998-251283/22.
XX
PT Liquefaction of starch for, e.g. production of sweeteners - comprises use
PT of enzyme hybrids including cellulose binding domain for starch.
XX
PS Example 8; Page 65-67; 83pp; English.
XX
CC This is the nucleotide sequence of the termamyl-linker-CBDEGV fusion
CC construct pNAMK6.1. This is an enzyme hybrid which can be used for the
CC liquefaction of starch. The enzyme hybrids contain amino acid sequences
CC of alpha-amylase linked to a cellulose binding domain (CBD). The CBD is
CC selected from the Bacillus or cellulomonas endoglucanase, C. xylanase A
CC or the Humicola insolens EGV sequence. The starch is liquefied by
CC treating, in aqueous medium, with such an enzyme hybrid. A recombinant
CC expression vector comprising a construct containing isolated DNA encoding
CC enzyme hybrids with amylolytic activity, promoter and stop signals can be
CC used to transform host cells for the production of the recombinant enzyme
CC hybrids. The enzyme hybrids are useful in industrial starch processing
CC especially for the production of sweeteners. Hybrid enzymes have altered
CC affinity for substrate and increased activity, resulting in at least 1 of
CC reduced calcium ion dependence, reduced formation of Maillard reaction
CC products and reduced effect of alpha-amylase on subsequent
CC saccharification

XX
SQ Sequence 6136 BP; 1475 A; 1545 C; 1712 G; 1404 T; 0 U; 0 Other;

Query Match   38.2%; Score 2017.2; DB 2; Length 6136;
Best Local Similarity 91.8%; Pred. No. 5.1e-297;
Matches 2203; Conservative   0; Mismatches 53; Indels 144; Gaps 1;

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Qy   2884  CAGCTGCATTAATGAATCGGCCAACCGCGGGGAGGCGGTTGCTATTGGGCGCTCT  2943
           ||| ||   ||||  ||||     |||||||||| ||||||||||| |||||||||
Db   4381  CATATGCGGTGTGAAATACCGCACAGAGAGAAATACCGCATCAGGCGGTCT  4322

Qy   2944  TCCGCTTCCTCGCTCACTGACTCGCTCGGTCGTTCGGCTCGGCGCGGAGCGGGTATCA  3003
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4321  TCCGCTTCCTCGCTCACTGACTCGCTCGGTCGTTCGGCTCGGCGCGGAGCGGGTATCA  4262

Qy   3004  GCTCACTCAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAAC  3063
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4261  GCTCACTCAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAAC  4202

Qy   3064  ATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTT  3123
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4201  ATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTT  4142

Qy   3124  TTCCATAGGCTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGG  3183
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4141  TTCCATAGGCTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGG  4082

Qy   3184  CGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGC  3243
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4081  CGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGC  4022

Qy   3244  TCTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGC  3303
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4021  TCTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGC  3962

Qy   3304  GTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCC  3363
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3961  GTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCC  3902

Qy   3364  AAGCTGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGGCTGCGCCTTATCCGTAAC  3423
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3901  AAGCTGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGGCTGCGCCTTATCCGTAAC  3842

Qy   3424  TATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGT  3483
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3841  TATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGT  3782

Qy   3484  AACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCT  3543
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3781  AACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCT  3722

Qy   3544  AACTACGGCTACACTAGAAGAACAGTATTTGGTATCCGCTCGCTCTGCTGAAGCCAGTTACC  3603
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3721  AACTACGGCTACACTAGAAGGACAGTATTTGGTATCCGCTCGCTCTGCTGAAGCCAGTTACC  3662

Qy   3604  TTCGGAAAAAGAGTTGGTAGCTTCTTGATCCGGCAAACAACCACCGCTGGTAGCGGTGGT  3663
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3661  TTCGGAAAAAGAGTTGGTAGCTTCTTGATCCGGCAAACAACCACCGCTGGTAGCGGTGGT  3602

Qy   3664  TTTTTTGTTTGCAAGCAGCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTG  3723
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3601  TTTTTTGTTTGCAAGCAGCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTG  3542

Qy   3724  ATCTTTTCTACGGGGTCTGACGCTCAGTGGAACGAAAACTCACGTTAAGGGATTTTGGTC  3783
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3541  ATCTTTTCTACGGGGTCTGACGCTCAGTGGAACGAAAACTCACGTTAAGGGATTTTGGTC  3482

Qy   3784  ATGAGATTATCGTCGACCAAAGCGGCCATGCTGCCTCCCCACTCCTGCAGTTCGGGGGCA  3843
           ||||||||||||||||||||||||||||||||||||||||||||||||
Db   3481  ATGAGATTATCAAAAAGGATCTTCACCTAGATCCTT--------------  3446

Qy   3844  TGGATGCGCGGATAGCCGCTCGTGGTTCCTGGATGCCGACGGATTTGCACTGCCGCGTAG  3903
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Db  3445  ------------------------------------------------------------ 3446
Qy  3904  AACTCCGGAGGTCGTCAGCGCTCAGCGACGAGCTGAACCAACTCGGCGAGGGGATCGAGC 3963
Db  3445  ------------------------------------------------------------ 3446
Qy  3964  CCGGGGTGGGCGAAGAACTCCAGCGACGATGAGATCGCCGGCGTCGGAGGATCATCCAGCCGGCGG 4023
Db  3445  TTGGGGTGGGCGAAGAACTCCAGCGACGATGAGATCGCCGGCGTCGGAGGATCATCCAGCCGGCGG 3386
Qy  4024  TCCCCGAAAACGATTCCGAAGCCCAACCTTTCATAGAGAGGCGGCGTGGAATCGAAAATCT 4083
Db  3385  TCCCCGAAAACGATTCCGAAGCCCAACCTTTCATAGAGAGGCGGCGTGGAATCGAAAATCT 3326
Qy  4084  CGTGATGGCAGGTTGGGCGTCGCTCATTCGAACCCCAGAGTCCCGCTCAGA 4143
Db  3325  CGTGATGGCAGGTTGGGCGTTCGGCGTCGGTCATTCGAACCCCAGAGTCCCGCTCAGA 3266
Qy  4144  AGAACTCGTCAAGAAGGCGATAGAAGGCGATGCGCTGCGAATCGGGAGGCGGCGATACCGT 4203
Db  3265  AGAACTCGTCAAGAAGGCGATAGAAGGCGATGCGCTGCGAATCGGGAGGCGGCGATACCGT 3206
Qy  4204  AAAGCACGAGGAAGCCGTCAGCCATTCGCCCGCAAGCTCTTCAGCAATATCACGGGTAG 4263
Db  3205  AAAGCACGAGGAAGCCGTCAGCCATTCGCCCGCAAGCTCTTCAGCAATATCACGGGTAG 3146
Qy  4264  CCAAGCGTATGCTTCTGATAGCGGTCCGCCACACCCCAGCCGGCCACAGTCGATGAATCCAG 4323
Db  3145  CCAAGCGTATGCTCCTGATAGCGGTCCGCCACACCCCAGCCGGCCACAGTCGATGAATCCAG 3086
Qy  4324  AAAAGCGGCCATTTTCCACCATGATATTCGGCAAGCAGGCATCGCCATGGGTCACGACGA 4383
Db  3085  AAAAGCGGCCATTTTCCACCATGATATTCGGCAAGCAGGCATCGCCATGTGTCACGACGA 3026
Qy  4384  GATCCTCGCCGTCGGGCATGCGCGCCTTGAGCCTGGCAACAGTTCGGCGTGGCGCGAGCC 4443
Db  3025  GATCCTCGCCGTCGGGCATGCGCGCCTTGAGCCTGGCAACAGTTCGGCGTGGCGCGAGCC 2966
Qy  4444  CCTGATGCTCTTCGTCCAGATCATCCTGATCGACAAGACCGGCTTCCATCCGAGTACGTG 4503
Db  2965  CCTGATGCTCTTCGTCCAGATCATCCTGATCGACAAGACCGGCTTCCATCCGAGTACGTG 2906
Qy  4504  CTCGCTCGATGCGATGTTTCGCTTGGTGGTCGAATGGGCAGGTAGCCGGATCAAGCGTAT 4563
Db  2905  CTCGCTCGATGCGATGTTTCGCTTGGTGGTCGAATGGGCAGGTAGCCGGATCAAGCGTAT 2846
Qy  4564  GCAGCCGCCGCATTGCATCAGCCATGATGGATACTTTCTCGGCAGGAGCAAGGTGAGATG 4623
Db  2845  GCAGCCGCCGCATTGCATCAGCCATGATGGATACTTTCTCGGCAGGAGCAAGGTGAGATG 2786
Qy  4624  ACAGGAGATCCGCCCCGGCACTTCGCCCAATAGCAGCCAGTCCCTTCCCGCTTCAGTGA 4683
Db  2785  ACAGGAGATCCGCCCCGGCACTTCGCCCAATAGCAGCCAGTCCCTTCCCGCTTCAGTGA 2726
Qy  4684  CAACGTCGAGCACAGCTGCCGCAAGGAACGCCCGTCGTGGCCAGCCACGATAGCCGCGCTG 4743
Db  2725  CAACGTCGAGCACAGCTGCCGCAAGGAACGCCCGTCGTGGCCAGCCACGATAGCCGCGCTG 2666
Qy  4744  CCTCGTCCTGCAGTTCATTCAGGGCACCGGACAGGTCGGTCTTGACAAAAAGAACCGGGC 4803
Db  2665  CCTCGTCCTGCAGTTCATTCAGGGCACCGGACAGGTCGGTCTTGACAAAAAGAACCGGGC 2606
Qy  4804  GCCCCTGCGCTGACAGCCGGAACACGGCGGCATCAGAGCAGCCGATTGTCTGTTGTGCCC 4863
Db  2605  GCCCCTGCGCTGACAGCCGGAACACGGCGGCATCAGAGCAGCCGATTGTCTGTTGTGCCC 2546
Qy  4864  AGTCATAGCCGAATAGCCTCTCCACCCAAGCGGCCGGAGAACCTGCGTGCAATCCATCTT 4923
Db  2545  AGTCATAGCCGAATAGCCTCTCCACCCAAGCGGCCGGAGAACCTGCGTGCAATCCATCTT 2486
Qy  4924  GTTCAATCATGCGAAACGATCCTCTCTTGATCAGATCTTGATCCCCTGCGCC 4983
Db  2485  GTTCAATCATGCGAAACGATCCTCATCCTGTCTCTTGATCAGATCTTGATCCCCTGCGCC 2426
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Qy  4984  ATCAGATCCTTGGCGGCGAAGAAGAAAGCCATCCAGTTTACTTGCGAGGGCTTCCAACCTTAC 5043
Db  2425  ATCAGATCCTTGGCGGCGAAGAAGAAAGCCATCCAGTTTACTTGCGAGGGCTTCCAACCTTAC 2366
Qy  5044  CAGAGGGCGCCCCAGTGGCAATTCCGGTTCGGCTTCGGCTTCGGTGTCTGCATAAAACCGCCAGTCTA 5103
Db  2365  CAGAGGGCGCCCCAGTGGCAATTCCGGTTCGGCTTCGGCTTCGGTGTCTGCATAAAACCGCCAGTCTA 2306
Qy  5104  GCTATCGCCATGTAAGCCACTGCAAGCTACCTGCTTCCTTCTTCGGCTTGCGTTTCCC 5163
Db  2305  GCTATCGCCATGTAAGCCACTGCAAGCTACCTGCTTCCTTCTTCGGCTTGCGTTTCCC 2246
Qy  5164  TTGTCCAGATAGCCCAGTAGCTGACATTCATCCGGGTCAGCACCGTTTCTGCGGACTGG 5223
Db  2245  TTGTCCAGATAGCCCAGTAGCTGACATTCATCCGGGTCAGCACCGTTTCTGCGGACTGG 2186
Qy  5224  CTTTCTACGTGTTCCGCTTCCTTTAGCAGCGCCCTTGCGCCCTGAGTGCTTGCGGCAGCGTG 5283
Db  2185  CTTTCTACGTGTTCCGCTTCCTTTAGCAGCGCCCTTGCGCCCTGAGTGCTTGCGGCAGCGTG 2126
```

RESULT 4
AAX52020/c
ID   AAX52020 standard; DNA; 4800 BP.
XX
AC   AAX52020;
XX
DT   18-JUN-1999 (first entry)
XX
DE   Synthetic DNA plasmid sequence synlux4.
XX
KW   DNA plasmid; lux A; lux B; Vibrio fisherii; luciferase; promoter;
KW   tn9 kanamycin/neomycin phosphotransferase; DNA synthesis;
KW   replication competent double-stranded polynucleotide; ss.
XX
OS   Synthetic.
XX
PN   WO9914318-A1.
XX
PD   25-MAR-1999.
XX
PF   16-SEP-1998;   98WO-US019312.
XX
PR   16-SEP-1997;   97US-0059017P.
XX
PA   (TEXA) UNIV TEXAS SYSTEM.
XX
PI   Evans GA;
XX
DR   WPI; 1999-244029/20.
XX
PT   Synthesis of replication competent double-stranded polynucleotides.
XX
PS   Example 4; Fig 4A-C; 135pp; English.
XX
CC   The present sequence represents a synthetic DNA plasmid sequence,
CC   designed using synthetic parts of known plasmids. Within the sequence are
CC   included the sequences of lux A, lux B, the A and B components of the
CC   Vibrio fisherii luciferase sequence, positions of pUC19 including the
CC   origin of replication and replication stability sequences, and the
CC   promoter and coding sequence for tn9 kanamycin/neomycin
CC   phosphotransferase. The plasmid was synthesised form 192 50-mers (see
CC   AAX5021-12) to demonstrate the method of the invention. The
CC   specification describes a method for the synthesis of replication
CC   competent double-stranded polynucleotides. The method comprises
CC   generating a first set of oligonucleotides corresponding to the plus
CC   strand and a second set corresponding to the minus strand and annealing.
CC   The method can be used for preparing polynucleotides encoding sequences
CC   involved in a biochemical pathway. In particular, they can be used to
CC   produce polynucleotides encoding enzymes, e.g. hexokinase, phosphohexose
CC   isomerase, phosphofructokinase-1, aldolase, triose-phosphate isomerase,
CC   glyceraldehyde-3-phosphate dehydrogenase, phosphoglycerate kinase,

CC   phosphoglycerate mutase, enolase or pyruvate kinase. They can also be
CC   used for the preparation of viral particles, artificial genomes and
XX   artificial genetic systems
SQ   Sequence 4800 BP; 1345 A; 1032 C; 1163 G; 1260 T; 0 U; 0 Other;

Query Match   33.9%; Score 1793.4; DB 2; Length 4800;
Best Local Similarity   91.8%; Pred. No. 4.4e-263;
Matches 1980; Conservative   0; Mismatches   0; Indels 176; Gaps   1;

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Qy   3127 CATAGGCTCCGCCCCCTGACGAGCATCACAAAAATGACGCTCAAGTCAGAGGTGGCGA 3186
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4800 CATAGGCTCCGCCCCCTGACGAGCATCACAAAAATGACGCTCAAGTCAGAGGTGGCGA 4741

Qy   3187 AACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCT 3246
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4740 AACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCT 4681

Qy   3247 CCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTG 3306
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4680 CCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTG 4621

Qy   3307 GCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAG 3366
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4620 GCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAG 4561

Qy   3367 CTGGGCTGTGTGCACGAACCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTTAACTAT 3426
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4560 CTGGGCTGTGTGCACGAACCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTTAACTAT 4501

Qy   3427 CGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAAC 3486
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4500 CGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAAC 4441

Qy   3487 AGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAAC 3546
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4440 AGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAAC 4381

Qy   3547 TACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTC 3606
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4380 TACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTC 4321

Qy   3607 GGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTT 3666
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4320 GGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTT 4261

Qy   3667 TTTGTTTGCAAGCAGCAGATTACGGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGATC 3726
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4260 TTTGTTTGCAAGCAGCAGATTACGGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGATC 4201

Qy   3727 TTTTCTACGGGGTCTGACGCTCAGTGGAACGAAAACTCACGTTAAGGGATTTTGGTCATG 3786
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4200 TTTTCTACGGGGTCTGACGCTCAGTGGAACGAAAACTCACGTTAAGGGATTTTGGTCAT- 4142

Qy   3787 AGATTATCGTCGACCAAAGCGGCCATCGTCGCCTGCCTCCTGCAGTTCGGGGGCATGG 3846
Db   4141 --------------------------------------------------------- 4142

Db   4141 --------------------------------------------------------- 4142
Qy   3847 ATGCCGCGGGATAGCCGGTCTTCCTGATGCCGCGACGGATTTGCACTGCGGTTAGAAAC 3906
Db   4141 --------------------------------------------------------- 4142

Qy   3907 TCCGGCGAGGTCGTTCAGCCTCCAGCCTCAGGCCAGCAGTCGGCAACCTCGCGAGGGGATCGAGCCCG 3966
          ||||
Db   4141 ------------------------------------------------------------GCCCG 4137

Qy   3967 GGGTGGGCGAAGAACTCCAGCATGAGATCCCGCGCTGGAGGATCATCCAGCCGGCGTCC 4026
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4136 GGGTGGGCGAAGAACTCCAGCATGAGATCCCGCGCTGGAGGATCATCCAGCCGGCGTCC 4077

Qy   4027 CGGAAAACGATTCCGAAGCCCACTGCAAGCTTCATAGAAGGCGGCGGTGGAATCGAAATCTCGT 4086
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4076 CGGAAAACGATTCCGAAGCCCACTGCAAGCTACCCACTGCTACTGGAAATCGAAATCTCGT 4017
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Qy   4087 GATGGCAGGTTGGGCGTCGCTTGGTCGGTCATTCGAACCCAGAGTCCGCTCAGAAGA 4146
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4016 GATGGCAGGTTGGGCGTCGCTTGGTCGGTCATTCGAACCCAGAGTCCGCTCAGAAGA 3957

Qy   4147 ACTCGTCAAGAAGGCGATAGAAGGCGATGGCGCTGCGAATCGGGAGCGGCGGCGATACCGTAAA 4206
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3956 ACTCGTCAAGAAGGCGATAGAAGGCGATGGCGCTGCGAATCGGGAGCGGCGGCGATACCGTAAA 3897

Qy   4207 GCACGAGGAAGGCGGTCAGCCCATTCGCCGCCAAGCTCTTCAGCAATATCACGGGTAGCCA 4266
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3896 GCACGAGGAAGGCGGTCAGCCCATTCGCCGCCAAGCTCTTCAGCAATATCACGGGTAGCCA 3837

Qy   4267 ACGCTATGTCCTGATAGCGGTCCGCCACACCCAGCCGGCCACAGTCGATGAATCCAGAAA 4326
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3836 ACGCTATGTCCTGATAGCGGTCCGCCACACCCAGCCGGCCACAGTCGATGAATCCAGAAA 3777

Qy   4327 AGCGGCCATTTTCCACCATGATATTCGGCAAGCAGGCATCGCCATGGGTCACGACGAGAT 4386
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3776 AGCGGCCATTTTCCACCATGATATTCGGCAAGCAGGCATCGCCATGGGTCACGACGAGAT 3717

Qy   4387 CCTCGCGCGTGGGCATGCGCGCCTTGAGCCTGGCGGTGGCGGAGCGCCTGGCGGAGCCCCT 4446
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3716 CCTCGCGCGTGGGCATGCGCGCCTTGAGCCTGGCGGTGGCGGAGCGCCTGGCGGAGCCCCT 3657

Qy   4447 GATGCTCTTCGTCCAGATCATCCTGATCGACAAGAACCGGCTTCCATCCGAGTACGTGCTC 4506
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3656 GATGCTCTTCGTCCAGATCATCCTGATCGACAAGAACCGGCTTCCATCCGAGTACGTGCTC 3597

Qy   4507 GCTCGATGGCGATGTTCGCTTGGTGGTCAGGCAGGTAGCGGCGGGGATCAAGCTATGCA 4566
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3596 GCTCGATGGCGATGTTCGCTTGGTGGTCAGGCAGGTAGCGGCGGGGATCAAGCTATGCA 3537

Qy   4567 GCCGCGCATTGCATCAGCCATGATGGATACTTTCTCGGAGGACCAAGGTGAGATGACA 4626
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3536 GCCGCGCATTGCATCAGCCATGATGGATACTTTCTCGGAGGACCAAGGTGAGATGACA 3477

Qy   4627 GGAGATCCTGCCCCCGGCACTTCGCCCAATAGCAGCAGTCCCCTTCCGCTTCAGTGACAA 4686
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3476 GGAGATCCTGCCCCCGGCACTTCGCCCAATAGCAGCAGTCCCCTTCCGCTTCAGTGACAA 3417

Qy   4687 CGTCGAGCACAGCAGTCGCGCGCAAGGAACCCCGTCGTGGCCAGCCACGACGATAGCGCGCTGCCT 4746
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3416 CGTCGAGCACAGCAGTCGCGCGCAAGGAACCCCGTCGTGGCCAGCCACGACGATAGCGCGCTGCCT 3357

Qy   4747 CGTCCTGCAGTTCATTCAGGGCACCGGACAGCAGTCGGTCTTGACAAAAAGAACCGGGGCC 4806
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3356 CGTCCTGCAGTTCATTCAGGGCACCGGACAGCAGTCGGTCTTGACAAAAAGAACCGGGCGC 3297

Qy   4807 CCTGCGCTGACAGCCGGAACAGCGGCATCAGAGCGCAGGCAGCCGATTGTCTGTTGTGCCCAGT 4866
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3296 CCTGCGCTGACAGCCGGAACAGCGGCATCAGAGCGCAGGCAGCCGATTGTCTGTTGTGCCCAGT 3237

Qy   4867 CATAGCCGGAATAGCCTTCCACCCAGGCGGCCGGGAGAACCTGCGTGCAATCCATCATCTTGTT 4926
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3236 CATAGCCGGAATAGCCTTCCACCCAGGCGGCCGGGAGAACCTGCGTGCAATCCATCATCTTGTT 3177

Qy   4927 CAATCATGCGAAACGATCCTCATCCGTCTTGATCGATCTTGATCCCCGCGCCATC 4986
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3176 CAATCATGCGAAACGATCCTCATCCGTCTTGATCGATCTTGATCCCCGCGCCATC 3117

Qy   4987 AGATCCTTGGCGCGGCAAGAAGCCATCCCAGTTTACTTTGCAGGGCTTCCCAACCTTACCAG 5046
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3116 AGATCCTTGGCGCGGCAAGAAAGCCATCCCAGTTTACTTTGCAGGGCTTCCAACCTTACCAG 3057

Qy   5047 AGGGCCGCCCCAGTCGGCCCCAGTCGCCAATTCCGGTTGCTTGCTCGTCGTCAATCATCTTAGCT 5106
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3056 AGGGCCGCCCCAGTCGGCCCCAGTCGCCAATTCCGGTTGCTTGCTCGTGTCCATAAAAACCGCCCAGTCTAGCT 2997

Qy   5107 ATCGCCATGTAAGCCCCACTGCAAGCTACCTCGTTTCTTTGCGCTTGCCGTTTCCCTTG 5166
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2996 ATCGCCATGTAAGCCCCACTGCAAGCTACCCGCAAGCTACCCGGCGCGTGCCGTTTCCCTTG 2937
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Qy  5167  TCCAGATAGCCCAGTAGCTGACATTCATCCCGGGTCAGCACCGTTTCTCGGGACTGGCTT  5226
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2936  TCCAGATAGCCCAGTAGCTGACATTCATCCCGGGTCAGCACCGTTTCTCGGGACTGGCTT  2877

Qy  5227  TCTACGGTGTTCCGCTTCCTTTAGCAGCCCTTGCGCCCTGAGTGCTTGCGGCAGCGTG    5283
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2876  TCTACGGTGTTCCGCTTCCTTTAGCAGCCCTTGCGCCCTGAGTGCTTGCGGCAGCGTG    2820
```

RESULT 5

AAV33629/c
ID   AAV33629 standard; DNA; 5594 BP.
XX
AC   AAV33629;
XX
DT   29-DEC-1998 (first entry)
XX
DE   GENSA 981, a monomeric DNA sequence produced by the invention.
XX
KW   Class IIS restriction endonuclease recognition site;
KW   endogenous mouse promoter element; tissue-specific gene expression;
KW   hormone-specific gene expression; 88;
KW   developmental-specific gene expression.
XX
OS   Synthetic.
XX
PN   WO9838326-A1.
XX
PD   03-SEP-1998.
XX
PF   28-FEB-1998;   98WO-US003918.
XX
PR   28-FEB-1997;   97US-0070910P.
XX
PA   (NATU-) NATURE TECHNOLOGY CORP.
XX
PI   Hodgson CP, Zink MA, Xu G;
XX
DR   WPI; 1998-495399/42.
XX
PT   Method for assembling gene or gene vector - comprises use of primers
PT   containing class IIS restriction endonuclease recognition sites.
XX
PS   Page 107-110; 141pp; English.
XX
CC   Example 2: Page 107-110; 141pp; English.
CC   The invention provides a novel method for directing self-assembly of a
CC   gene having three or more fragments in a directionally and spatially
CC   ordered fashion to produce a gene or a gene vector. The method involves
CC   usage of primers, containing class IIS restriction endonuclease
CC   recognition sites, for isolation of these fragments. As described in the
CC   disclosure, the method may also use a vector for the incorporation and
CC   screening of endogenous mouse promoter elements for the identification of
CC   cell specific promoters. In the example given, plasmids pBK-CMV
CC   (AAV33626), pVLMB (AAV33623) and pVLOVhGH-900 (AAV33621) were used as
CC   templates from which six fragments were amplified. Each of the fragments
CC   contained different regulatory sequences. The six PCR fragments were
CC   designed to self-assemble into a retro-vector using the method of the
CC   invention. The present sequence, designated as GENSA 981, represents the
CC   monomeric DNA sequence of the six ligated fragments. In general, the
CC   method is claimed to be useful for isolating and identifying regulatory
CC   sequences from a cell, including those for enhanced biological activity,
CC   or tissue-specific, hormone-specific or developmental-specific gene
CC   expression
XX
SQ   Sequence 5594 BP; 1232 A; 1519 C; 1518 G; 1325 T; 0 U; 0 Other;

Query Match   31.3%; Score 1652.4; DB 2; Length 5594;
Best Local Similarity   85.4%; Pred. No. 1e-241;
Matches 1916; Conservative   0; Mismatches 261; Indels 67; Gaps   4;

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Qy  3167  GCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCTG  3226
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5531  GCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCTG  5472

Qy  3227  GAAGCTCCCTGCGCGCTCTCCTGTTCCGACCCTGCCGCTTACGGATACCTGTCCGCGCT  3286
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5471  GAAGCTCCCTGCGCGCTCTCCTGTTCCGACCCTGCCGCTTACGGATACCTGTCCGCGCT  5412

Qy  3287  TTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGTATCTCAGTTCGG  3346
          ||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Db  5411  TTCTCCCTTCGGGAAGCGTGGCGCTTTCTCAATGCTCACGCTGTAGTATCTCAGTTCGG  5352

Qy  3347  TGTAGGTCGTTCGCTCCAAGTGGGCGTGTGTGCACGAACCCCCGTTCAGCCCGACCGCT  3406
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5351  TGTAGGTCGTTCGCTCCAAGTGGGCGTGTGTGCACGAACCCCCGTTCAGCCCGACCGCT  5292

Qy  3407  GCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCAC  3466
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5291  GCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCAC  5232

Qy  3467  TGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGT  3526
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5231  TGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGT  5172

Qy  3527  TCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTC  3586
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5171  TCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTC  5112

Qy  3587  TGCTGAAGCCAGTTACCTTGATCCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAACCA  3646
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5111  TGCTGAAGCCAGTTACCTTGATCCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAACCA  5052

Qy  3647  CCGCTGTAGCCGGTGTTTTTTGTTTGCAAGCAGCAGATTACGCGCAGAAAAAAAGGAT  3706
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5051  CCGCTGTAGCCGGTGTTTTTTGTTTGCAAGCAGCAGATTACTGGCGCCCGAGTGAGG  4992

Qy  3707  CTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTCACGCTC--------AGTGGAACG  3757
          ||||||||||||||||||||||||||||||||||||||||        |||||||||
Db  4991  GGTTGTGGCCTCTTTTATTGAGTCTCGGGGAGCAGAGCGCGCGCAACAGAAGCGAGAAGCG  4932

Qy  3758  AAAACTCACGTTAAGGGATTTGGTCATGAGATTATCGTCGACCAAAGGCGCCATCGTGC  3817
          ||||                  ||  |||  | ||||||     |     ||||
Db  4931  AACTGATTGGTTAGTTCAAATAAGGCACAGCAGGTCATTCAGTCTTCAGCCACCCTGGA  4872

Qy  3818  CTC----------CCCACTCTGCAGTTCGGGGGCATGGAGCCGGATAGCCGCTG  3864
          |||          |||  |
Db  4871  AACATCTGATGGTTCTCTAGAAACTGCTAGAAACTGGGGACCATCTGTT  4812

Qy  3865  CTGGTTTCCTGGATGCGACGGATTTGC--------ACTGCCGGTAGAACTCCGCGAG  3914
          ||||||||| ||||||||||||||              ||||||||||||||||||
Db  4811  CTTGGCCCTGAGCCGGCAGGAACTGCTTACCACAGATCCTGTTTGGCCCCATATTCA  4752

Qy  3915  GTCGTCCAGCTTCAGGCGCTGAACCAACTCGCGAGGGGGATCGAGCCGCGGGGTGGGC  3974
          |   | ||| ||||   |           ||  |  ||     ||||||  |   ||
Db  4751  GCTGTTCCATCTGTTCTTGGCCCTGAGCCGGGCAGGAACTGCTTACCACAGATATCCTG  4692

Qy  3975  GAAGAACTCCAGCATGAGATCCCGCGCTGGAGGATCATCCAGCCGCGTCCGGAAAAC  4034
          |||| |||||  ||    ||| ||||   ||||   |||||   ||||   |||||
Db  4691  TTTGGCCCATATTCAGCTGTTCAGCCTTGACCCTTGTCTTCGATCGAACTTCTATTCTC  4632

Qy  4035  GATTCGGAAGCCCAACCTTTCATAGAGAGGCGCGGTGGAATCGAAATCTCG--------  4085
          ||||||    || |||      ||| |   ||| |   ||||    ||
Db  4631  AGTTATGTATTTTTCATGCCTTGCAAAATGGCGTTACTTAAGCTAGCTTGCCAAACCTA  4572

Qy  4086  -------------------TGATGGCAGGTTGGGCGTTCGCTTGGTTCGGTCATT  4119
                             ||||||  | ||||||||  ||||||||||||||
Db  4571  CAGGTGGGGTCTTTCATTCCCCCGTTTTTCTGGAGGTGGGCGTTGGGTTCGGTCATT  4512

Qy  4120  TCGAACCCCAGAGTCCCGCTCAGAAGAACTCGTCAGAAGGCGATGAGGCGATGCGCT  4179
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4511  TCGAACCCCAGAGTCCCGCTCAGAAGAACTCGTCAGAAGGCGATGAGGCGATGCGCT  4452

Qy  3107  CCGGCGTTGCTGGCGTTTTTCCATAGCTCCGCCCCCCTGACGAGCATCACAAAAATCGAC  3166
          |||||||||||| |||||||| ||||||||||||||||||||||||||||||||||||||
Db  5591  CGGCGTTGCTGCTGGCGTTTTTCATAGCTCCGCCCCCCTGACGAGCATCACAAAAATCGAC  5532
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Qy   4180 GCGAATCGGGAGCGGCGATACCGTAAAGACGAGGAAGCCGGTCAGCCCATTCGCGCCAA 4239
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4451 GCGAATCGGGAGCGGCGATACCGTAAAGACGAGGAAGCCGGTCAGCCCATTCGCGCCAA 4392

Qy   4240 GCTCTTCAGCAATATCACGGGTAGCCAAGCTATGTCCTGATAGCGGTCCGCCACACCCA 4299
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4391 GCTCTTCAGCAATATCACGGGTAGCCAAGCTATGTCCTGATAGCGGTCCGCCACACCCA 4332

Qy   4300 GCCGGCCACAGTCGATGAATCCAGAAAAGCGGCCATTTTCCACCATGATATTCGGCAAGC 4359
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4331 GCCGGCCACAGTCGATGAATCCAGAAAAGCGGCCATTTTCCACCATGATATTCGGCAAGC 4272

Qy   4360 AGGCATCGCCATGGGTCACGACGAGATCCTCGCCCGTCGGGCATGCGCGCCTTGAGCCTG 4419
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4271 AGGCATCGCCATGGGTCACGACGAGATCCTCGCCCGTCGGGCATGCGCGCCTTGAGCCTG 4212

Qy   4420 CGAACAGTTCGGCTGGCGCGAGCCCCTGATGCTCTTCGTCCAGATCATCCTGATCGACAA 4479
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4211 CGAACAGTTCGGCTGGCGCGAGCCCCTGATGCTCTTCGTCCAGATCATCCTGATCGACAA 4152

Qy   4480 GACCGGCTTCCATCCGAGTACGTGCTCGCTCGATGGTTTCGTTGGTCGTCGAATG 4539
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4151 GACCGGCTTCCATCCGAGTACGTGCTCGCTCGATGGTTTCGTTGGTCGTCGAATG 4092

Qy   4540 GGCAGGTAGCCGGATCAAGGCTATGCAGCGCCGATTGCATCAGCGCCATGATGGATACTT 4599
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4091 GGCAGGTAGCCGGATCAAGGCTATGCAGCGCCGATTGCATCAGCGCCATGATGGATACTT 4032

Qy   4600 TCTCGGCAGGAGCAAGGTGAGATGACAGGAGATCCTCGCCCCGGCACTTCGCCCAATAGCA 4659
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4031 TCTCGGCAGGAGCAAGGTGAGATGACAGGAGATCCTCGCCCCGGCACTTCGCCCAATAGCA 3972

Qy   4660 GCCAGTCCCTTCCCGCTTCAGTGACAACGTCGAGCACAGCTGCGCGAAGGAACGCCCGTCG 4719
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3971 GCCAGTCCCTTCCCGCTTCAGTGACAACGTCGAGCACAGCTGCGCGAAGGAACGCCCGTCG 3912

Qy   4720 TGGCCAGCCACGATAGCCGGCGCTGCCGGTTCATTCAGGCGCACCGGACAGGT 4779
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3911 TGGCCAGCCACGATAGCCGGCGCTGCCGGTTCATTCAGGCGCACCGGACAGGT 3852

Qy   4780 CGGTCTTGACAAAAAGAACCGGGAGCGGCCCCTGCGCTGACAGCCGGAACACGGCGCATCAG 4839
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3851 CGGTCTTGACAAAAAGAACCGGGAGCGGCCCCTGCGCTGACAGCCGGAACACGGCGCATCAG 3792

Qy   4840 AGCAGCCGATTGTCTTGTGTTGCCAGTCATAGCCTTCCACCCAAGCGGCCG 4899
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3791 AGCAGCCGATTGTCTTGTGTTGCCAGTCATAGCCTTCCACCCAAGCGGCCG 3732

Qy   4900 GAGAACCTGCGTGCAATCCATCTTGTTCAATCATGCGAAACGATCCTCATCCTGTCTCTT 4959
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3731 GAGAACCTGCGTGCAATCCATCTTGTTCAATCATGCGAAACGATCCTCATCCTGTCTCTT 3672

Qy   4960 GATCAGATCTTGATCCCCTGCGCGCCATCAGATCCTTGGGCGGCAAGAAAGCCATCCAGTTTA 5019
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3671 GATCAGATCTTGATCCCCTGCGCGCCATCAGATCCTTGGGCGGCAAGAAAGCCATCCAGTTTA 3612

Qy   5020 CTTTGCAGGGCTTCCCAACCTTACCAGAGGGCGCCCCAGCTGGCAATTCCGGTTCGCTTG 5079
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3611 CTTTGCAGGGCTTCCCAACCTTACCAGAGGGCGCCCCAGCTGGCAATTCCGGTTCGCTTG 3552

Qy   5080 CTGTCATAAAACCGCCACCGTCTAGCTATCGCAATGTAAGCCCACTGCGAAGCTACCTGCT 5139
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3551 CTGTCATAAAACCGCCACCGTCTAGCTATCGCAATGTAAGCCCACTGCGAAGCTACCTGCT 3492

Qy   5140 TTCTCTTTGGCGTTGCGTTTTCCCTTGTCCAGATAGCCCAGTAGCTGACATTCATCCGGG 5199
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3491 TTCTCTTTGGCGTTGCGTTTTCCCTTGTCCAGATAGCCCAGTAGCTGACATTCATCCGGG 3432

Qy   5200 GTCAGCACCGTTTCTGCGGACTGGCTTTCTACGTGTTCCGCCTTTTTAGCAGCCCTTGC 5259
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3431 GTCAGCACCGTTTCTGCGGACTGGCTTTCTACGTGTTCCGCCTTTTTAGCAGCCCTTGC 3372

Qy   5260 GCCCTGAGTGCTTGCGGCAGCGTG 5283
          ||||||||||||||||||||||||
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Db   3371 GCCCTGAGTGCTTGCGGCAGCGTG 3348

RESULT 6
ADJ71288/c
ID   ADJ71288 standard; DNA; 4245 BP.
XX
AC   ADJ71288;
XX
DT   06-MAY-2004 (first entry)
XX
DE   PCR-BluntII-TOPO cloning vector containing M13 primers.
XX
KW   ds; vector; DNA amplification; sequencing; collapsible emulsion.
XX
OS   Synthetic.
XX
PN   WO2003106678-A1.
XX
PD   24-DEC-2003.
XX
PF   13-JUN-2003; 2003WO-AU000746.
XX
PR   13-JUN-2002; 2002AU-00002981.
XX
PA   (NUCL-) NUCLEICS PTY LTD.
XX
PI   Tillett D, Thomas T;
XX
DR   WPI; 2004-191031/18.
XX
PS   Disclosure; Fig 1; 11lpp; English.
XX
CC   The present invention relates to a method of performing a chemical
CC   reaction between reactants, which involves subjecting an emulsion
CC   comprising a discontinuous first phase in which at least one of the
CC   reactants is present, and a continuous second phase, to a physical or
CC   chemical change such that a continuous phase is formed from the
CC   discontinuous phase, and providing conditions in which the chemical
CC   reaction between the reactants takes place. A system for carrying out the
CC   method is also disclosed. The method is useful for performing a chemical
CC   reaction between reactants, where the chemical reaction is chosen from
CC   DNA sequencing, PCR, rolling circle amplification (RCA), ligase chain
CC   reaction (LCR), rapid amplification of cDNA ends (RACE), reverse-
CC   transcriptase PCR (RT-PCR), DNA fingertyping, DNA genotyping,
CC   endonuclease-restriction digest, DNA ligation, DNA phosphorylation, DNA
CC   methylation, DNA labeling, RNA digestion, proteolytic digestion, and
CC   protein modification. The protein modification is glycosylation or
CC   phosphorylation or the chemical reaction is DNA sequencing or PCR. The
CC   present sequence is a cloning vector used in the exemplification of the
CC   invention.
XX
SQ   Sequence 4245 BP; 1031 A; 1076 C; 1147 G; 991 T; 0 U; 0 Other;

Query Match   30.9%; Score 1634.4; DB 12; Length 4245;
Best Local Similarity   80.6%; Pred. No. 5.6e-239;
Matches 2082; Conservative   0; Mismatches 211; Indels 291; Gaps 3;

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Qy   2942 CTTCCGCTTCCTCGCTCACTGACTCCGCTCGGTCGTTCGGCTGCGCTCGGCGGCCGAGCCGGTAT 3001
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4245 CTTCCGCTTCCTCGCTCACTGACTCCGCTCGGTCGTTCGGCTGCGCTCGGCGGCCGAGCCGGTAT 4186

Qy   3002 CAGCTCACTCAAAGGCGGTAATACGGGGATAACGCAGGAAAGA 3061
          |||||||||||||||||||||||||||||||||||||||||||
Db   4185 CAGCTCACTCAAAGGCGGTAATACGGGGATAACGCAGGAAAGA 4126

Qy   3062 ACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGT 3121
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4125 ACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGT 4066

Qy   3122 TTTTCCATAGGCTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGT 3181
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db   4065 TTTTCCATAGGCTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGT 4006
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   3182 GGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTGCGTGC 3241
Db   4005 GGCGAAACCCGACACAGGACTACTAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTGCGTGC 3946

Qy   4137 TCGCTTGTCTCGGTCATTTGCAGTTGCATGAGCGGGGATACATATTTGAATGTATTTAGAAAATAAACAAATAG 2866
Db   2925 AGGGTTATTGTCTCATGAGCGGGGATACATATTTGAATGTATTTAGAAAATAAACAAATAG

Qy   4137 ---------------------------
Db   2865 GGGTTCCGGCGCACATTTCCCCGAAAAGTGCCACCTGTATGCGGTGTGAAATACCGCACAG 2806

Qy   4150 -----------------CTCAGAAGAACTC
Db   2805 ATGCGTAAGGAGAGAAAATACCGCATCAGGAAAATTGTAAGCGTTAATAATTCAGAGAACTC 2746

Qy   4210 GTCAAGAAGGCGATAGAAGGCGATGCGCTGCGAATCGGAGCGGCGATACCGTAAAGCAC 4151
Db   2745 GTCAAGAAGGCGATAGAAGGCGATGCGCTGCGAATCGGAGCGGCGATACCGTAAAGCAC 2686

Qy   4270 GAGGAAGCGGGTCAGCCCATTCGCCGCCAAGCTCTTCAGCAATATCACGGGTAGCCAACGC 4211
Db   2685 GAGGAAGCGGGTCAGCCCATTCGCCGCCAAGCTCTTCAGCAATATCACGGGTAGCCAACGC 2626

Qy   4330 TATGTCCTGATAGCGGTCCGCCACACCCAGCCGGCCACAGTCGATGAATCCAGAAAAGCG 4271
Db   2625 TATGTCCTGATAGCGGTCCGCCACACCCAGCCGGCCACAGTCGATGAATCCAGAAAAGCG 2566

Qy   4390 GCCATTTTCCACCATGATATTCGGCAAGCAGGCATCGGCCATGGTCACGACAGATCCTC 4331
Db   2565 GCCATTTTCCACCATGATATTCGGCAAGCAGGCATCGGCCATGGTCACGACGAGATCCTC 2506

Qy   4450 GCCGTCGGCATGCGCGCCTTGAGCCTGGCGGCCGGACCAGTTCGGCTGGCCGGAGCCCCTGATG 4391
Db   2505 GCCGTCGGGCATGCGCGCCTTGAGCCTGGCAACAGTTCGGCTGGCCGGAGCCCCTGATG 2446

Qy   4510 CTCTTCGTCCAGATCATCCTGATCGACAAGACCGGCTTCCATCCCGAGTACGTCGCTC 4451
Db   2445 CTCTTCGTCCAGATCATCCTGATCGACAAGACCGGCTTCCATCCCGAGTACGTCGCTC 2386

Qy   4570 GATGCGATGTTTCGCTTGGTGTGTCGAATGGGCAGGTAGCCGGATCAAGCGTATGCAGCCG 4511
Db   2385 GATGCGATGTTTCGCTTGGTGTGTCGAATGGGCAGGTAGCCGGATCAAGCGTATGCAGCCG 2326

Qy   4630 CCGCATTGCATCAGCCATGATGGATACTTTCTCGGCAGGAGCAAGGTGAGATGACAGGAG 4571
Db   2325 CCGCATTGCATCAGCCATGATGGATACTTTCTCGGCAGGAGCAAGGTGAGATGACAGGAG 2266

Qy   4690 ATCCTGCCCGCACTTCGCCCAATAGCAGCCAGTCCCTTCCGCTTCAGTGACAACGTC 4631
Db   2265 ATCCTGCCCGCACTTCGCCCAATAGCAGCCAGTCCCTTCCGCTTCAGTGACAACGTC 2206

Qy   4750 GAGCACAGCTGCGCAAGGAACGCCCGTCGTGGCCAGCCACGATAGCCGCGCTGCCTCGTC 4691
Db   2205 GAGCACAGCTGCGCAAGGAACGCCCGTCGTGGCCAGCCACGATAGCCGCGCTGCCTCGTC 2146

Qy   4810 CTGCAGTTCATTCAGGGCACCGGACAGGTCGGTCTTGACAAAAAGAACCGGCGGCCCCTG 4751
Db   2145 TTGCAGTTCATTCAGGGCACCGGACAGGTCGGTCTTGACAAAAAGAACCGGCGGCCCCTG 2086

Qy   4870 CGGCTGACAGCCGGAACACGGGCGGCATCAGAGCAGCCGATTGTCTGTTGTGCCCAGTCATA 4811
Db   2085 CGGCTGACAGCCGGAACACGGGCGGCATCAGAGCAGCCGATTGTCTGTTGTGCCCAGTCATA 2026

Qy   4930 GCCGAATAGCCTCTCCACCCAAGCGGCCGGAGAACCTGCGTGCAATCCATCTTGTTCAAT 4871
Db   2025 GCCGAATAGCCTCTCCACCCAAGCGGCCGGAGAACCTGCGTGCAATCCATCTTGTTCAAT 1966

Qy   4990 CATGCCGAAACGATCCTCATCCTGTCTCTTGATCAGATCTTGATCAGAT 4931
Db   1965 CATGCCGAAACGATCCTCATCCTGTCTCTTGATCAGATCTTGATCAGAT 1906

Qy   5050 CCTTGGCGCGAAGAAGCCATCCAGTTTACTTTGCAGGGCTTCCCAACCTTACCAGAGGG 4991
Db   1905 CCTTGGCGCGAGAAGAAGCCATCCAGTTTACTTTGCAGGGCTTCCCAACCTTACCAGAGGG 1846
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Qy  5051 CGCCCAGCTGGCAATTCCGGTTCGGTTGCTGCTGTCCATAAAACCGCCCAGTCTAGCTATCG 5110
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1845 CGCCCAGCTGGCAATTCCGGTTCGGTTGCTGCTGTCCATAAAACCGCCCAGTCTAGCTATCG 1786

Qy  5111 CCATGTAAGCCCACTGCAAGCTACCTGCTTTCTCTTTGCGCTTGCCTTGTTTCCCTTGTCCA 5170
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1785 CCATGTAAGCCCACTGCAAGCTACCTGCTTTCTCTTTGCGCTTGCCTTGTTTCCCTTGTCCA 1726

Qy  5171 GATAGCCCAGTAGCTGACATTCATCCGGGGTCAGCACCGTTTCTCGGACTGGCTTTCTA 5230
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1725 GATAGCCCAGTAGCTGACATTCATCCGGGGTCAGCACCGTTTCTCGGACTGGCTTTCTA 1666

Qy  5231 CGTG 5234
         ||||
Db  1665 CGTG 1662


RESULT 7
AAH74865/c
ID   AAH74865 standard; DNA; 5285 BP.
XX
AC   AAH74865;
XX
DT   29-OCT-2001  (first entry)
XX
DE   Nucleotide sequence of a construct comprising the PCV Rep gene.
XX
KW   Rolling circle replication; RCR; Rep gene; gene function; Geminivirus;
KW   Circovirus; Nanovirus; gene therapy; PCV; ss.
XX
OS   Synthetic.
OS   Porcine circovirus.
XX
PN   WO20161024-A2.
XX
PD   23-AUG-2001.
XX
PF   15-FEB-2001; 2001WO-US005394.
XX
PR   16-FEB-2000; 2000US-00505477.
XX
PA   (LARG-) LARGE SCALE BIOLOGY CORP.
XX
PI   Palmer KE, Pogue GP;
XX
DR   WPI; 2001-522601/57.
XX
PT   New polynucleotide capable of rolling circle replication in host, useful
PT   for discovery of gene function, comprises Rep genes, sequences that are
PT   cis on the polynucleotide and open reading frame encoding protein of
PT   interest.
XX
PS   Example 1; Fig 5; 61pp; English.
XX
CC   The specification describes a polynucleotide that is capable of rolling
CC   circle replication (RCR) in an eukaryotic host. The polynucleotide
CC   comprises a Rep gene encoding from a virus, sequences that are cis on the
CC   polynucleotide such that the Rep protein can bring about RCR of the
CC   polynucleotide, an open reading frame encoding a protein of interest
CC   capable of being expressed in the host, and optionally a multiple cloning
CC   site, where the polynucleotide lacks genes of the virus. The virus is
CC   selected from the group of genera of family Geminiviridae, Circoviridae
CC   and Nanovirus. The polynucleotide sequence is useful for the discovery of
CC   the function of genes in eukaryotic hosts, and for inducing or enhancing
CC   a trait in a host eukaryotic cell, for down-regulating a gene in a plant
CC   or in mammalian cell and thus altering or even eliminating the function
CC   of that gene, as gene sequence delivery tools for mammalian genomic
CC   approaches, for gene therapy applications (for delivering therapeutic or
CC   complementing gene products to organisms or cells), and in whole animal
CC   genomics. The present sequence represents a construct comprising the
CC   whole PCV genome. This construct contains the PCV Rep gene under the
CC   transcriptional control of its own promoter, and has the putative coat
CC   protein inactivated by insertion of the bacterial cloning vector


XX
SQ   Sequence 5285 BP; 1216 A; 1277 C; 1514 G; 1278 T; 0 U; 0 Other;

Query Match             30.9%;  Score 1634.4;  DB 4;  Length 5285;
Best Local Similarity   80.6%;
Matches 2082;  Conservative    0;  Mismatches  211;  Indels  291;  Gaps  3;
          Pred. No. 5.5e-239;

Qy  2942 CTTCCGCTTCCTCGCTCACTGACTCGCTGCGCTCGGCTGCTTCGGCTGCGGCGGAGCCGGTAT 3001
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5285 CTTCCGCTTCCTCGCTCACTGACTCGCTGCGCTCGGCTGCTTCGGCTGCGGCGGAGCCGGTAT 5226

Qy  3002 CAGCTCACTCAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGAAAAGA 3061
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5225 CAGCTCACTCAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGAAAAGA 5166

Qy  3062 ACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGT 3121
         ||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Db  5165 ACATGTGAGCAAAAGGCCAGCAAAAGCCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGT 5106

Qy  3122 TTTTCCATAGGCTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGT 3181
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5105 TTTTCCATAGGCTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGT 5046

Qy  3182 GGCGAAACCCGACAGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGC 3241
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5045 GGCGAAACCCGACAGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGC 4986

Qy  3242 GCTCTCCTGTTCCGACCCTGCCGCTTACCGGATATCCAGTTCGGTGTAGGTCGTTCGCT 3301
         ||||||||||||||||||||||||||||||||||  |||||||||||||||||||||||
Db  4985 GCTCTCCTGTTCCGACCCTGCCGCTTACCGGATATCCAGTTCGGTGTAGGTCGTTCGCT 4926

Qy  3302 GCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCAGTTCGGTGTAGGTCGTTCGCT 3361
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4925 GCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCAGTTCGGTGTAGGTCGTTCGCT 4866

Qy  3362 CCAAGTCTGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTA 3421
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4865 CCAAGTCTGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTA 4806

Qy  3422 ACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTG 3481
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4805 ACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTG 4746

Qy  3482 GTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGC 3541
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4745 GTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGC 4686

Qy  3542 CTAACTACGGCTACACTAGAAGAACAGTATTGGTATCCGCCTCTGCTGCGAAGCCAGTTA 3601
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4685 CTAACTACGGCTACACTAGAAGAACAGTATTGGTATCCGCCTCTGCTGCGAAGCCAGTTA 4626

Qy  3602 CCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTG 3661
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4625 CCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTG 4566

Qy  3662 GTTTTTTTGTTTGCAAGCAGCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTT 3721
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4565 GTTTTTTTGTTTGCAAGCAGCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTT 4506

Qy  3722 TGATCTTTTCTACGGGGTCTGACGCTCAGTGGAACGAAAACTCACGTTAAGGGATTTTGG 3781
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4505 TGATCTTTTCTACGGGGTCTGACGCTCAGTGGAACGAAAACTCACGTTAAGGGATTTTGG 4446

Qy  3782 TCATGAGATTATC----------------------------------------------- 3794
         |||||||||||||
Db  4445 TCATGAGATTATCAAAAAGGATCTTCACCTAGATCCTTTAAATTAAAAATGAAGTTTTA 4386

Qy  3795 ------------------------------------------------------GTCGACCA 3802
                                                                ||| |||
Db  4385 GCACGTGTCAGTCCTGCTCCTCGGCCACGAAGTGCACGCAGTTGCCGGCCGGGTGCCGGCA 4326

Qy  3803 AAGCCGGCCATCGTGCCTCCCCACTCCTGCAGTTCGGGGGCATGGAGTGCGCGGATAGCCGC 3862
         |||  |||     ||              |||             ||   ||
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Db 4325 GGGCGAACTCCGCCCCACGGCGTGCTCGCCGATCTCGGTCATGGCCGGCCGGAGGCGT 4266

Qy 3863 TGCTGGTTTCCTGGATGCCGACGGATTTGCACTGCCGGTAGAACTCCGCGAGGTCGTCCA 3922

Db 4265 CCCGGAAGTTCGTGGACACGACCTCCGACCACTCGGCCGTACAGCTCGTCGCCAGGCCGCA 4206

Qy 3923 GCC--- 3925

Db 4205 CCCACACCCAGGCCAGGGTGTGTCCGGCACCACCTGGTCCTGGACCGCGCTGATGAACA 4146

Qy 3926 ---TCAGGCAGCAGCTGAACCAACTCGGCAGGGGGATCGAGCCCGGGGTGGGCGAAGAACT 3982

Db 4145 GGGTCACGTCGTCCCCGGACCACACCGGCGAAGTCGTCTCCACGAGTCCCGGGAGAACC 4086

Qy 3983 CCAGCATGAGATCCCGCGTGGAGGATCATCCAGCCGGCGTCCCGAAAACGATTCCGA 4042

Db 4085 CGAGCCGGCCGTCGGTCCAGAACTCGACCCTCCGGCGTCGCGCCGACGGCGTGAGCGCCGAA 4026

Qy 4043 AGCCCAACCTTTCATAGAAGGGCGGTGGAATCGAAATCTCGTGATGGCCAGGTTGGGCG 4102

Db 4025 CGGCACTGGTCAACTTGGCCCATGGTGCCCTTCCTCACGTGCTGCTATTATTGAAGCATTTATC 3966

Qy 4103 TCGCTTGGTCGGTCATTTGAACCCCAGAGTCCCG--------------------- 4137

Db 3965 AGGGTTATTGTCTCTATGAGCCGGATACATATTTGAATGTATTTAGAAAAATAAACAAATAG 3906

Qy 4138 ------------------------------------ 4137

Db 3905 GGGGTTCCGGCCACATTTCCCGAAAAGTGCCACCTGTGTGAAATACCGCACAG 3846

Qy 4138 ----------------------CTCAGAAGAACTC 4150

Db 3845 ATGGCTAAGGAGAGAAAATACCGCATCAGGAAAATTGTAAGCGTTAATAATTCAGAAGAACTC 3786

Qy 4151 GTCAAGAAGGCGGATAGAAGGCGGATGGCGCTGGCGAATCGGCGGCGGCGATACCGTAAAGCAC 4210

Db 3785 GTCAAGAAGGCGGATAGAAGGCGGATGGCGCTGGCGAATCGGCGGCGGCGATACCGTAAAGCAC 3726

Qy 4211 GAGGAAGCGGGTCAGCCCATTCGCCGCCAAGCTCTTCAGCAATATCACGGGTAGCCAACGC 4270

Db 3725 GAGGAAGCGGGTCAGCCCATTCGCCGCCAAGCTCTTCAGCAATATCACGGGTAGCCAACGC 3666

Qy 4271 TATGTCCTGATAGCCGGTCCGCCACACCCAGCCGCCACAGTGATGAATCCAGAAAAGCG 4330

Db 3665 TATGTCCTGATAGCCGGTCCGCCACACCCAGCCGCCACAGTGATGAATCCAGAAAAGCG 3606

Qy 4331 GCCATTTTCCACCATGATATTCGGCAAGCAGCATCGCCATGGGTCACGACGAGATCCTC 4390

Db 3605 GCCATTTTCCACCATGATATTCGGCAAGCAGCATCGCCATGGGTCACGACGAGATCCTC 3546

Qy 4391 GCCGTCGGGCATGCGCGCCTTGAGCCTGGCGAACAGTTCGGCTGGCGGCGAGCCCCTGATG 4450

Db 3545 GCCGTCGGGCATGCGCGCCTTGAGCCTGGCGAACAGTTCGGCTGGCGGCGAGCCCCTGATG 3486

Qy 4451 CTCTTCGTCCAGATCATCGATCGACAAGACCGGCTTCCATCCGAGTACGTGCTCGCTC 4510

Db 3485 CTCTTCGTCCAGATCATCGATCGACAAGACCGGCTTCCATCCGAGTACGTGCTCGCTC 3426

Qy 4511 GATGGCGATGTTTCGCTTGGTCGTCGAATGGGTCAGGTAGCGGATCAAGCCTATGCAGCCG 4570

Db 3425 GATGGCGATGTTTCGCTTGGTCGTCGAATGGGTCAGGTAGCGGATCAAGCCTATGCAGCCG 3366

Qy 4571 CCGCATTGCATCAGCCATGATGGATACTTTCTCGGCGAGGATCAAGGTCGAGATGACCAGGAG 4630

Db 3365 CCGCATTGCATCAGCCATGATGGATACTTTCTCGGCGAGGATCAAGGTCGAGATGACCAGGAG 3306

Qy 4631 ATCCTGCCCCGGCACTTCGCCCAATAGCAGCCAGTCCCTTCCCGCTTCCGCGCTC 4690

Db 3305 ATCCTGCCCCGGCACTTCGCCCAATAGCAGCCAGTCCCTTCCCGCTTCCGCGCTC 3246

Qy 4691 GAGCACAGCTGCGCAAGGAACGCCCGTCGTGGCCAGCCACGATAGCCGCTGCTCGTC 4750

Db 3245 GAGCACAGCTGCGCAAGGAACGCCCGTCGTGGCCAGCCACGATAGCCGCTGCTCGTC 3186

Qy 4751 CTGCAGTTCATTCAGGCGACCAGGCACCGGACACAGTCGGTCTTGACAAAAAGAACCGGGCGGCCCCTG 4810

Db 3185 TTGCAGTTCATTCAGGGCACCGGACACAGGTCGGTCTTGACAAAAAGAACCGGGCGGCCCCCTG 3126

Qy 4811 CGCTGACAGCCCGGAACACGGCGGCCATCAGAGCAGCCGATTGTGTCGTTGTGCCCAGTCATA 4870

Db 3125 CGCTGACAGCCCGGAACACGGCGGCCATCAGAGCAGCCGATTGTCTGTTGTGCCCAGTCATA 3066

Qy 4871 GCCGAATAGCCTCTCCACCCAAGCGGCCGGAGAACCTCGTGCAATCCATCTTGTTCAAT 4930

Db 3065 GCCGAATAGCCTCTCCACCCAAGCGGCCGGAGAACCTCGTGCAATCCATCTTGTTCAAT 3006

Qy 4931 CATGGCGAAACGATCCTCATCGTGTCTTGATCAGATCTTGATCCCCTGCGCCATCAGAT 4990

Db 3005 CATGGCGAAACGATCCTCATCGTGTCTTGATCAGATCTTGATCCCCTGCGCCATCAGAT 2946

Qy 4991 CCTTGGGCGGCAAGAAAGCCATCCAGTTTACTTTGCAGGGCTTCCCAACCTTACCAGAGGG 5050

Db 2945 CCTTGGGCGGCAAGAAAGCCATCCAGTTTACTTTGCAGGGCTTCCCAACCTTACCAGAGGG 2886

Qy 5051 CGCCCCAGCTGGCAATTCCGGTTCGCTTCGTCGTCCATAAAACCGCCAGTCTAGCTATCG 5110

Db 2885 CGCCCCAGCTGGCAATTCCGGTTCGCTTCGTCGTCCATAAAACCGCCAGTCTAGCTATCG 2826

Qy 5111 CCATGTAAGCCACTGCGAAGCTACCTGCTTTCTCTTTGCGCTTGCGTTTCCCTTGTCCA 5170

Db 2825 CCATGTAAGCCACTGCGAAGCTACCTGCTTTCTCTTTGCGCTTGCGTTTCCCTTGTCCA 2766

Qy 5171 GATAGCCCAGTAGCTGACATTCATCGGGGTCAGCACCGTTTCGCGGACTGCTTTCTA 5230

Db 2765 GATAGCCCAGTAGCTGACATTCATCCGGGGTCAGCACCGTTTCGCGGACTGCTTTCTA 2706

Qy 5231 CGTG 5234

Db 2705 CGTG 2702

PS
XX   Example 7; SEQ ID NO 10; 147pp; English.
CC   The present sequence is that of vector pCR-XL-TOPO-CMV-pur-attB, which
CC   was used in an example from the invention to demonstrate phiC31 integrase
CC   -mediated integration into the chicken genome. The invention provides
CC   methods for using bacteriophage phiC31 integrase to integrate a
CC   heterologous polynucleotide into the genome of an avian cell. In this
CC   phage integrase-mediated integration method, a plasmid vector bearing a
CC   transgene and including the attB recognition sequence for the phage
CC   integrase is used. The vector, with integrase-coding mRNA, a vector
CC   expressing the integrase, or the integrase protein itself, are delivered
CC   into cells or embryos. The integrase recognises DNA sequences in the
CC   avian genome similar to attP sites, termed pseudo-attP sites, and mediates
CC   recombination between attB and pseudo-attP sites, resulting in the
CC   permanent integration of the transgene into the avian genome. The
CC   invention also provides: a genetically transformed avian; a method of
CC   producing a polypeptide; a polypeptide of interest expressed by a
CC   genetically transformed avian cell or its progeny; an avian egg; white
CC   comprising a heterologous polypeptide; an avian egg comprising a
CC   heterologous polypeptide; a method for generating a genetically modified
CC   avian cell or its progeny using a tagged chromosome; a genetically
CC   modified avian cell; and a modified avian chromosome comprising a lac
CC   operator region and a recombination site. The methods are useful in
CC   genetically transforming an avian cell for expressing, in large yields
CC   and at low cost, a wide range of desired proteins including those used as
CC   human and animal pharmaceuticals, diagnostics or livestock feed
CC   additives.
XX
SQ   Sequence 6233 BP; 1372 A; 1745 C; 1746 G; 1370 T; 0 U; 0 Other;

Query Match   30.9%; Score 1634.4; DB 13; Length 6233;
Best Local Similarity   80.6%;
Matches 2082;   Pred. No. 5.4e-239;
Conservative   0; Mismatches 211; Indels 291; Gaps 3;

Qy   2942 CTTCCGCTTCCTCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCCGGTAT 3001
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   6233 CTTCCGCTTCCTCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCCGGTAT 6174

Qy   3002 CAGCTCACTCAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGA 3061
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   6173 CAGCTCACTCAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGA 6114

Qy   3062 ACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGT 3121
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   6113 ACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGT 6054

Qy   3122 TTTTCCATAGGCTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGT 3181
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   6053 TTTTCCATAGGCTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGT 5994

Qy   3182 GGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGC 3241
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5993 GGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGC 5934

Qy   3242 GCTCTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAA 3301
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5933 GCTCTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAA 5874

Qy   3302 GCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCT 3361
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5873 GCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCT 5814

Qy   3362 CCAAGCTGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTA 3421
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5813 CCAAGCTGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTA 5754

Qy   3422 ACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTG 3481
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5753 ACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTG 5694

Qy   3482 GTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGC 3541
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5693 GTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGC 5634

Qy   3542 CTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTTCTGCTGAAGCCAGTTA 3601
          |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db   5633 CTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCGCTCTGCTGAAGCCAGTTA 5574

Qy   3602 CCTTCGGAAAAAGAGTTGGTAGCTCTTGATCGGCAAACAACAACCACCGCTGGTAGCGGTG 3661
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5573 CCTTCGGAAAAAGAGTTGGTAGCTCTTGATCGGCAAACAACAACCACCGCTGGTAGCGGTG 5514

Qy   3662 GTTTTTTTGTTTGCAAGCAGCAGATTACGGCGCAGAAAAAAAGGATCTCAAGAAGATCCTT 3721
          ||||||||||||||||||||||||||||||||||||||||| |||||||||||||||||||
Db   5513 GTTTTTTTGTTTGCAAGCAGCAGATTACGGCGCAGAAAAAAAAGGATCTCAAGAAGATCCTT 5454

Qy   3722 TGATCTTTTCTACGGGGTCTGACGCTCAGTGGAACGAAAACTCACGTTAAGGGATTTTGG 3781
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5453 TGATCTTTTCTACGGGGTCTGACGCTCAGTGGAACGAAAACTCACGTTAAGGGATTTTGG 5394

Qy   3782 TCATGAGATTATC--- 3794
          |||||||||||||
Db   5393 TCATGAGATTATCAAAAAGGATCTTCACCTAGATCCTTTTAAATTAAAAATGAAGTTTTA 5334

Qy   3795 --GTCGACCA 3802
                                                            ||||||||
Db   5333 GCACGGTGTCAGTCTCTGTCCTCCCCCACGCGAGCGTGCACGCAGTGCCGGCCGGGTCGCGCA 5274

Qy   3803 AAGGCGGCCATCGTGCCTCCCCACTCCTGCAGTTCGGGGGGCATGGATGCGCGGATAGCCGC 3862
          ||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5273 GGGGGGAACTCCGGCCCCAGCCCCCACGCGTGCTCGGTCGGCATCGTGGCCGAGGTCGTCCA 5214

Qy   3863 TGCTCGTTTCCTGATGCCGACGATTTGCACTGCGTAGGTAGAACTCCGCGAGGTCGTCCA 3922
          ||||||||||||||||||||||||||||||||||||||
Db   5213 CCCGGAAGTTCGTGCGACACCGACCCTCGGCGTACGACCTCGGCGTCGTCCAGGCCGCGCA 5154

Qy   3923 GCC 3925
          |||
Db   5153 CCCACACCCAGGCCAGGGTGTTGTCCGGCACCACCTGGTCCTGGACCGGCGTGGGCGATGAACA 5094

Qy   3926 --TCAGGCAGCGTGAACCAACTCGCGGGATCGAGCCCGGGTGGGGCCGAAGAACT 3982
             ||| ||||||| ||||||| |||||||||||||||||||||||||||
Db   5093 GGGTCACGTCGTCCGGAGTCGTCCTCCAGGAGTCGTCCTCCGGAGACCGGGAGACC 5034

Qy   3983 CCAGCATGAGATCCCGCGCTGGAGGATCATCCAGCCGGCGTCCCGGGAAAACGATTCCGA 4042
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5033 CGAGCCGGTCGGTCCGGTTCCAGAACTCGACCGCTCCGGCGACGTCGCGCGGGTGAGCAGGGAA 4974

Qy   4043 AGCCCAACCTTTCATAGAAGGCGGCGGTGGTGGAATCGAAATCTCGTGATGGCAGGTTGGGCG 4102
          ||||| ||||| ||| ||||| ||||||||||| |||
Db   4973 CGGCACTGGTCAACTTGGCCATGGTGCCCTCCTCACGTGCTGTTATTATTGAAGCATTTATC 4914

Qy   4103 TCGCTTGGTCGGTCATTTCGAACCCCAGAGTCCCG------ 4137
          | | | |||||
Db   4913 AGGGTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACAAATAG 4854

Qy   4137 -- 4137
Db   4853 GGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGTATGCGGTGTGAAATACCGCACAG 4794

Qy   4138 ------------------------------------CTCAGAAGACTC 4150
                                              ||||||||||||
Db   4793 ATGCGTAAGGAGAAAATACCGCATCAGGAGAAAATTGTAAGCGTTAATATTCAGAAGAACTC 4734

Qy   4151 GTCAAGAAGGCGATAGAAGGCGATGCGCTGCGAATCGGGAGCGGCGATACCGTAAAGCAC 4210
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4733 GTCAAGAAGGCGATAGAAGGCGATGCGCTGCGAATCGGGAGCGGCGATACCGTAAAGCAC 4674

Qy   4211 GAGGAAGCGGTCAGCCCATTCGCCGCCAAGCTCTTCAGCAATATCACGGGTAGCCAACGC 4270
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4673 GAGGAAGCGGTCAGCCCATTCGCCGCCAAGCTCTTCAGCAATATCACGGGTAGCCAACGC 4614

Qy   4271 TATGTCCTGATAGCGGTCCGCCACACCCAGCCGGCCACAGTCGATGAATCCAGAAAAGCG 4330
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4613 TATGTCCTGATAGCGGTCCGCCACACCCAGCCGGCCACAGTCGATGAATCCAGAAAAGCG 4554

```
Qy  4331 GCCATTTCCACCATGATATTCGGCAAGCAGGCATCGCCATGGGTCACGACGAGATCCTC 4390
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4553 GCCATTTCCACCATGATATTCGGCAAGCAGGCATCGCCATGGGTCACGACGAGATCCTC 4494

Qy  4391 GCCGTCGGGCATGCCGCGCCTTGAGCCTGGCGGCGGCCGAGCCCCTGATG 4450
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4493 GCCGTCGGGCATGCTCGCGCCTTGAGCCTGGCGGCGGCCGAGCCCCTGATG 4434

Qy  4451 CTCTTCGTCCAGATCATCCTGATCGACAAGACCGGCTTCCATCCGAGTACGTGCTCGCTC 4510
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4433 CTCTTCGTCCAGATCATCCTGATCGACAAGACCGGCTTCCATCCGAGTACGTGCTCGCTC 4374

Qy  4511 GATGGCGATGTTCGCTTGGTGGTCGAATGGGCAGGTAGCCGGATCAAGCGTATGCAGCCG 4570
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4373 GATGGCGATGTTCGCTTGGTGGTCGAATGGGCAGGTAGCCGGATCAAGCGTATGCAGCCG 4314

Qy  4571 CCGGATTGCATCAGCCATGATGGAATACTTTCTCGGCGAGGAGCAAGGTGAGATGACAGGAG 4630
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4313 CCGGATTGCATCAGCCATGATGGAATACTTTCTCGGCGAGGAGCAAGGTGAGATGACAGGAG 4254

Qy  4631 ATCCTGCCCCGCACTTCGCCCAATAGCAGCCAGTCCCTTCCGCGCTTCAGTGACAACGTC 4690
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4253 ATCCTGCCCCGGCACTTCGCCCAATAGCAGCCAGTCCCTTCCGCGCTTCAGTGACAACGTC 4194

Qy  4691 GAGCACAGCTGCCAAGGAACGCCGTCGTGCCAGCCACGATAGCCGGCGCTGCCTCGTC 4750
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4193 GAGCACAGCTGCGCAAGGAACGCGGCCCCGTCGTGCCAGCCACGATAGCCGCGCGCTGCCTCGTC 4134

Qy  4751 CTGCAGTTCATTCAGGGCACCCGACAGGTCGGTCTTGACAAAAAGAACCCGGGCGCCCCTG 4810
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4133 TTGCAGTTCATTCAGGGCACCCGACAGGTCGGTCTTGACAAAAAGAACCCGGGCGCCCCTG 4074

Qy  4811 CGCTGCAGCCGGAACACGGCGGCATCAGAGCAGCCGATTGTCTGTGTGCCCAGTCATA 4870
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4073 CGCTGACAGCCGGAACACGGCGGCATCAGAGCAGCCGATTGTCTGTTGTGCCCAGTCATA 4014

Qy  4871 GCCGAATAGCCTCTCCACCCAAGCGGCCGAGAACCTGCGTGCAATCCATCTTGTTCAAT 4930
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4013 GCCGAATAGCCTCTCCACCCAAGCGGCCGAGAACCTGCGTGCAATCCATCTTGTTCAAT 3954

Qy  4931 CATGGCGAAAGATCCTCATCCTGTCTTCTTGATCAGATCTTGATCCCCTGCGCCATCAGAT 4990
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3953 CATGGCGAAACGATCCTCATCCTCGTCTTCTTGATCAGAGCTTCAGACTCCCTGCGCCATCAGAT 3894

Qy  4991 CCTTGGCGGCAAGAAAGCCATCCAGTTACTTGCAGGGCTTCCAACCTTACCAGAGGGG 5050
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3893 CCTTGGCGGCGGAGAAAGCCATCCAGTTACTTGCAGGGCTTCCAACCTTACCAGAGGGG 3834

Qy  5051 CGCCCCAGCTGGCAATTCCGGTTCGCTTGCGTCCATAAAACCGGCCCAGTCTAGCTATCG 5110
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3833 CGCCCCAGCTGGCAATTCCGGGTTCGCTTGCGTGTCCATAAAACCGGCCCAGTCTAGCTATCG 3774

Qy  5111 CCATGTAAGCCCACTGCAAGCTACCCTGCTTTCTCTTTGCGCTTGGCTTTCCCTTGTCCA 5170
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3773 CCATGTAAGCCCACTGCAAGCTACCCTGCTTTCTCTTTGCGCTTGGCTTTCCCTTGTCCA 3714

Qy  5171 GATAGCCCAGTAGCTGACATTCATCCGGGGTCAGCACCGGTTCTGCGGACTGGCTTTCTA 5230
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3713 GATAGCCCAGTAGCTGACATTCATCCGGGGTCAGCACCGGTTCTGCGGACTGGCTTTCTA 3654

Qy  5231 CGTG 5234
         ||||
Db  3653 CGTG 3650
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RESULT 9
ABX94355/c
ID   ABX94355 standard; DNA; 5285 BP.
XX
AC   ABX94355;
XX
DT   19-JUN-2003 (first entry)
XX

DE   Rolling circle replicon construct 1.
XX
KW   Virucide; vaccine; gene therapy; Rep gene; rolling circle replication;
KW   Construct 1; PCV; ds.
XX
OS   Porcine circovirus.
OS   Simian virus 40.
OS   Synthetic.
XX
PN   US2002187952-A1.
XX
PD   12-DEC-2002.
XX
PF   20-DEC-2001; 2001US-00038001.
XX
PR   16-FEB-2000; 2000US-00505477.
XX
PA   (PALM/) PALMER K E.
PA   (POGU/) POGUE G G.
PA   (MCCO/) MCCORMICK A.
XX
PI   Palmer KE, Pogue GG, Mccormick A;
XX
DR   WPI; 2003-341042/32.
XX
PT   New rolling circle DNA replicons or polynucleotides, useful in vaccine or
PT   gene therapy applications, for eliciting an immunization reaction in a
PT   eukaryotic host, or for inducing or enhancing a function or trait in a
PT   host eukaryotic cell.
XX
PS   Example 1; Fig 5; 51pp; English.
XX
CC   The invention relates to a polynucleotide capable of eliciting an
CC   immunisation reaction in a eukaryotic host to a peptide or polypeptide.
CC   The polynucleotide encodes the peptide or polypeptide, and contains
CC   elements of a viral genome (i.e. the Rep gene) that is capable of rolling
CC   circle replication. The peptide or polypeptide is capable of expression
CC   in the eukaryotic host. Also included are constructing a polynucleotide
CC   capable of eliciting an immunisation reaction in a host (comprising
CC   inserting a sequence encoding a peptide or polypeptide into the
CC   polynucleotide, where the polynucleotide comprises elements of a viral
CC   genome that is capable of rolling circle replication) and immunising a
CC   host comprising administering a composition comprising the polynucleotide
CC   into the host. Substantially higher levels of IgG antibody induction were
CC   seen in mice injected with immunogenic protein insert linked to a rolling
CC   circle replication cassette versus immunogenic protein inserted into a
CC   non-rolling circle replicon mammalian expression vector. Levels of IgG
CC   antibody through successive bleeds were higher for both luciferase and
CC   beta-galactosidase expression cassettes linked to a porcine Circovirus
CC   cassette, as compared to non-rolling circle replicon linked vectors or
CC   injection with saline alone, vector without insert, purified luciferase
CC   or beta-galactosidase. The polynucleotide capable of rolling circle
CC   replication in a eukaryotic host is useful in vaccine or gene therapy
CC   applications, or for eliciting an immunisation reaction in a eukaryotic
CC   host. The rolling circle replicons or polynucleotides are also useful for
CC   the discovery of the function of genes in eukaryotic hosts, for inducing
CC   or enhancing a function or trait in a host eukaryotic cell, or for down-
CC   regulating a gene in a plant or mammalian cells, which alters or even
CC   eliminates the function of that gene. The ancillary protein is useful for
CC   potentiating an immunisation reaction in the host elicited by the peptide
CC   or polypeptide. The present sequence (termed Construct 1) is a
CC   polynucleotide of the invention comprising the whole PCV (porcine
CC   cirovirus) cloned into the Invitrogen cloning vector pCR BLUNT II-TOPO.
CC   The PCV Rep gene is under control of its own promoter and the coat
CC   protein gene is inactivated by insertion of the vector
XX
SQ   Sequence 5285 BP; 1216 A; 1276 C; 1515 G; 1278 T; 0 U; 0 Other;

Query Match   30.9%; Score 1632.8; DB 8; Length 5285;
Best Local Similarity   80.5%; Pred. No. 9.6e-239;
Matches 2081;   Conservative   0; Mismatches 212; Indels 291; Gaps   3;

Qy   2942 CTTCCGCTTCCTCGCTCACTGACTCCGTCGCGCTCCGCTCGTCGTTCGGCGTGCGGCGAGCGGTAT 3001

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Db  4205  CCCACACCCAGGCCAGGGTGTGTCCGGCACCACCTGGTCCTGCGACCGCGCTGATGAACA  4146
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  5285  CTTCCGGCTTCCTCGCTCACTGACTCGCTGCGGTCGGCTCGGCGTCGGCGTGCGGCGTAT  5226

Db  3926  ---TCAGGCAGCAGCTGAACCAACTCGCGAGGGGATCGAGCCCGGGGATGGGCGAAGAACT  3982
          |||||||||||||||||||||||
Qy  3002  CAGCTCACTCAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGA  3061

Db  4145  GGGTCACTCACCACCCGCGAGTCGTCCTCCGAAGTCGTCCCGGGCAGGAACGATTCCGA-  4086
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  5225  CAGCTCACTCAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGA  5166

Db  3983  CCAGCATGAGATCCCCGCGTGGAGCATCATCCGCGGCGCGTCCCGGAAACGATTCCGA-  4042
          |||||||||||||||||||||||||||||||
Qy  3062  ACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGT  3121

Db  4085  CGAGCGCGGTCGGTCCAGAACTGCACCGCTCCGGCGACGTGCGCGGGTGAGCACCGGAA  4026
          | ||||||||||||||||||||||||||||||||
Qy  5165  ACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGGCGT  5106

Db  4043  AGCCCAACCTTTCATAGAAGGCGGCGTGAATCGAAATCTCGTGATGCAGCAGGTTGGGCG  4102
          |||||||||||||||||||||||||||
Qy  3122  TTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAATCGACGCTCAAGTCAGAGGT  3181

Db  4025  CGGCACTGGTCAACTTGGCATGGTGGGCCCTCCTCACGTGCGCTATTATTGAAGCATTTATC  3966
          |||||||||||||||||||||||||||||
Qy  5105  TTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAATCGACGCTCAAGTCAGAGGT  5046

Db  4103  TCGCTTGGTGGTCATTTCGAACCCCAGAGTCCG----------  4137
          |||||||||||||||||||||||
Qy  3182  GGGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGC  3241

Db  3965  AGGGTTATTGTCTCATGAGCGGGGATACATATTTGAATGTATTTAGAAAAAATAAACAAATAG  3906
          --------
Qy  5045  GGGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGC  4986

Db  4138  -------------------------------  4137
          
Qy  3242  GCTCTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGCT  3301

Db  3905  GGGGTTCCGCGCACATTTCCCGCAAAAGTGCCACCTGTGTGAAATACCGCACAG------CTCAGAAGAACTC  3846
          ||||||||
Qy  4985  GCTCTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGGAA  4926

Db  4138  -----------------CTCAGAAGAACTC  4150
          |||||||||||||
Qy  3302  GCGGTGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCT  3361

Db  3845  ATGCGTAAGGAGAAAATACCGCATCAGGAATTGTAAGCGTTAATAATTCAGAAGAACTC  3786
          ||||||||||||||||||||||||||||||||||||||||||
Qy  4925  GCGGTGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCT  4866

Db  4151  GTCAAGAAGCGGATAGAAGGCGATGCGCTGCGAATCGGGAGGCGGCGATACCGTAAAGCAC  4210
          |||||||||||||||||||||||||||||||
Qy  3362  CCAAGCTGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTA  3421

Db  3785  GTCAAGAAGCGGATAGAAGGCGATGCGCTGCGAATCGGGAGGCGGCGATACCGTAAAGCAC  3726
          ||||||||||||||||||||||||||||||||||||||||||||
Qy  4865  CCAAGCTGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTA  4806

Db  4211  GAGGAAGCGGTCAGCCATTCGCCGCCAAGCTCTTCAGCAATATCACGGGTAGCCAACGC  4270
          ||||||||||||||||||||||||||||||||
Qy  3422  ACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTG  3481

Db  3725  GAGGAAGCGGTCAGCCATTCGCCGCCAAGCTCTTCAGCAATATCACGGGTAGCCAACGC  3666
          ||||||||||||||||||||||||||||||||||||||
Qy  4805  ACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTG  4746

Db  4271  TATGTCCTGATAGCGGTCCCGGCCACACCCCAGCCGGCCACAGTCGATCGAATCCAGAAAGCG  4330
          ||||||||||||||||||||||||||||||||
Qy  3482  GTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGC  3541

Db  3665  TATGTCCTGATAGCGGTCCCGGCCACACCCCAGCCGGCCACAGTCGATCGAATCCAGAAAGCG  3606
          ||||||||||||||||||||||||||||||||
Qy  4745  GTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGC  4686

Db  4331  GCCATTTTCACCATGTATATTCGGCAAGCAGCAGCCAGTCATCGCCATGGGTCACGACGAGATCCTC  4390
          ||||||||||||||||||||||||||||||||
Qy  3542  CTAACTACGGCTACACTAGAAGAACAGTATTGGTATCTGCGCTCTGCTGAAGCCAGTTA  3601

Db  3605  GCCATTTTCACCATGTATATTCGGCAAGCAGCAGCCAGTCATCGCCATGGGTCACGACGACATCCTC  3546
          ||||||||||||||||||||||||||||||||
Qy  4685  CTAACTACGGCTACACTAGAAGGACAGTATTGGTATCTGCGCTCTGCTGAAGCCAGTTA  4626

Db  4391  GCCGTCGGGCATGCGCGCCTTGAGCGTCGGCGGCGAACAGTTCGGCTGGCGCGAGCCCGTGATG  4450
          |||||||||||||||||||||||||||||||
Qy  3602  CCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTG  3661

Db  3545  GCCGTCGGGCATGCGCGCCTTGAGCGTCGGCGGCGAACAGTTCGGCTGGCGCGAGCCCGTGATG  3486
          ||||||||||||||||||||||||||||||||
Qy  4625  CCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTG  4566

Db  4451  CTCTTCGTCCAGATCATCCTGATCGACAAGACCGGCTTCCATCCGGATCAAGGGTACGTGCTCGCTC  4510
          |||||||||||||||||||||||||||||||
Qy  3662  GTTTTTTTGTTTGCAAGCAGCAGATTACGGCGCAGAAAAAAAGGATCTCAAGAAGATCCTT  3721

Db  3485  CTCTTCGTCCAGATCATCCTGATCGACAAGACCGGCTTCCATCCGGATCAAGGGTACGTGCTCGCTC  3426
          ||||||||||||||||||||||||||||||||
Qy  4565  GTTTTTTTGTTTGCAAGCAGCAGATTACGGCGCAGAAAAAAAGGATCTCAAGAAGATCCTT  4506

Db  4511  GATGCGATGTTTCGCTTGGTGGTCGAATGGGCAGGTAGCCGGATCAAGCGTATGCAGCCG  4570
          ||||||||||||||||||||||||||||||||
Qy  3722  TGATCTTTTTCTACGGGGTCTGACGCTCAGTGGAACGAAAACTCACGTTAAGGGATTTTGG  3781

Db  3425  GATGCGATGTTTCGCTTGGTGGTCGAATGGGCAGGTAGCCGGATCAAGCGTATGCAGCCG  3366
          ||||||||||||||||||||||||||||||||
Qy  4505  TGATCTTTTTCTACGGGGTCTGACGCTCAGTGGAACGAAAACTCACGTTAAGGGATTTTGG  4446

Db  4571  CCGATTGCATCAGCCATGATGGATACTTTCTCGGCAGGAGCAAGGTGAGATGACAGGAG  4630
          
Qy  3782  TCATGAGATTATC-------------------------  3794

Db  3365  CCGATTGCATCAGCCATGATGGATACTTTCTCGGCAGGAGCAAGGTGAGATGACAGGAG  3306
          ||||||||||
Qy  4445  TCATGAGATTATCAAAAAGGATCTTCACCTAGATCCTTTTAAATTAAAAATGAAGTTTTA  4386

Db  4631  ATCCTCGCCCCGGCCACTTCGCCCAATAGCAGCCAGTCCCTTCCCGCTTCAGTGACAACGTC  4690
          -----------GTCGACCA
Qy  3795  ----------------------------GTCGACCA  3802

Db  3305  ATCCTCGCCCCGGCCACTTCGCCCAATAGCAGCCAGTCCCTTCCCGCTTCAGTGACAACGTC  3246
          ||||||||||||||||||||||||||||||||
Qy  4385  GCACGTGTCAGTCCTGCTCGGCTCCCACTCGTGCACGAACCGCAGCGTTGCCGGGGTCGCA  4326

Db  4691  GAGCACAGTCGCGCAAGGGAAGGACACGCCCGTCGTGGCCAGCCAGATAGCCGCCCTCGTC  4750
          ||||||||||||||||||||||||||||||||
Qy  3803  AAGGCGGCCATCGTCGTGCACCTGCCGCTGTCGGGGCATGGGATGCGGCGGATAGCCGC  3862

Db  3245  GAGCACAGTCGCGCAAGGGAAGGACACGCCCGTCGTGGCCAGCCAGATAGCCGCCCTCGTC  3186
          ||||||||||||||||||||||||||||||||
Qy  4325  GCACGTGTCAGTCCTGCTCGGCTCCCACTCGTGCACGAACCGCAGCGTTGCCGGGGTCGCA  4266

Db  4751  CTGCAGTTCATTCAGGGCACCGGACAACTCGTAGAACTCCGCCAGTCGTCCA  4810
          ||||||||||||||||||||||||||||||||
Qy  3863  TGCTCGGTTTCCTGATGCCACGCCGATTTCGCTGCGGTAGAACTCCGGACGTCTCATCC  3922

Db  3185  TTTGCAGTTCATTCAGGGCACCGGAGTAGAACTCCGGACGTCTCATCC  3126
          ||||||||||||||||||||||||||||||||
Qy  4265  CCCGGAAGTTCGTGACACGACACCTTCGCGTACAGTCGTCGGTACAGGCGGCGCA  4206

Db  4811  CGCTGACAGCCGGAACACGGCGCATCAGCAGCCGATTGTCTGTTGTGCCCAGTCATA  4870
          ||||||||||||||||||||||||||||||||
Qy  3923  GCC--------------------------------  3925

Db  3125  CGCTGACAGCCGGAACACGGCGCATCAGCAGCCGATTGTCTGTTGTGCCCAGTCATA  3066
          |||
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CC   cell specific promoters. In the example given, plasmid VLSNO2, containing
CC   a circularly permuted mouse VL30 genome, was used in the construction of
CC   single long terminal repeat (LTR) vectors used in the method of the
CC   invention. In general, the method is claimed useful for isolating and
CC   identifying regulatory sequences from a cell, including those for
CC   enhanced biological activity, or tissue-specific, hormone-specific or
CC   developmental-specific gene expression
XX
SQ   Sequence 6561 BP; 1629 A; 1593 C; 1696 G; 1643 T; 0 U; 0 Other;

Query Match   30.6%;   Score 1618.2;   DB 2;   Length 6561;
Best Local Similarity   86.7%;   Pred. No. 1.5e-236;
Matches 1911;   Conservative   0;   Mismatches 23;   Indels 269;   Gaps   1;

Qy 3081 GCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTCCATAGGCTCCGCC 3140
Db 2305 GCAGGTGACTCGAGGCGGCGCATCGGCGTTGCTGGCGTTTTCCATAGGCTCCGCCC 2246

Qy 3141 CCCTGACGAGCATCACAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACT 3200
Db 2245 CCCTGACGAGCATCACAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACT 2186

Qy 3201 ATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTGCGCTCTCCTGTTCCGACCCT 3260
Db 2185 ATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTGCGCTCTCCTGTTCCGACCCT 2126

Qy 3261 GCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAG 3320
Db 2125 GCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCAATG 2066

Qy 3321 CTCACGCTGTAGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTGCA 3380
Db 2065 CTCACGCTGTAGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTGCA 2006

Qy 3381 CGAACCCCCCGTTCAGCCCGTTGCGCCTTATCGGTAACTATCGTCTTGAGTCAA 3440
Db 2005 CGAACCCCCCGTTCAGCCCGTTGCGCCTTATCCGTAACTATCCTCTTGAGTCCAA 1946

Qy 3441 CCCGGTAAGACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGC 3500
Db 1945 CCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGC 1886

Qy 3501 GAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAG 3560
Db 1885 GAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAG 1826

Qy 3561 AAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGG 3620
Db 1825 AAGGACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGG 1766

Qy 3621 TAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTGTTTGCAAGCA 3680
Db 1765 TAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTGTTTGCAAGCA 1706

Qy 3681 GCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTC 3740
Db 1705 GCAGATTACG 1696

Qy 3741 TGACGCTCAGTGGAACGAAAACTCACGTTAAGGGATTTTGGTCATGAGATTATCGTGAC 3800
Db 1695 -------------------------------------------------------- 1696

Qy 3801 CAAAGGCCGGCCATCGTGCCTCCCCACTCCTGCCAGTTCGGGGGCATGCAGGGGATAGCC 3860
Db 1695 -------------------------------------------------------- 1696

Qy 3861 GCTGCGTGGTTCCTGGATGCCGAGCTGGATTTGCACTGCGCGGTAGAACTCCGCCGAGGTCGTC 3920
Db 1695 -------------------------------------------------------- 1696

Qy 3921 CAGCCTCAGGCAGCAGCAACTCGCGAGGGGATCGAGCCCGGGGTGGGCGAAGAA 3980
Db 1695 -----------------------------AATTCCGGGGTGGGCGAAGAA 1675
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Qy 4871 GCCGAATAGCCTCTCCACCCAAGCGGCCGGAGAACCTGCGTGCAATCCATCTTGTTCAAT 4930
Db 3065 GCCGAATAGCCTCTCCACCCAAGCGGCCGGAGAACCTGCGTGCAATCCATCTTGTTCAAT 3006

Qy 4931 CATGCGGAAACGATCCTCATCCTGTCTCTTGATCAGATCTTGATCCCCTGCGGCCATCAGAT 4990
Db 3005 CATGCGGAAACGATCCTCATCCTGTCTCTTGATCAGAGCTTGATCAGAGCTTGATCCCCTGCGGCCATCAGAT 2946

Qy 4991 CCTTGGCGCGCAAGAAAGCCATCCAGTTTACTTGCAGGGGCTTCCCAACCTTACCAGAGGG 5050
Db 2945 CCTTGGCGCGGAGAAAGCCGAGAAAGCCATCCAGTTTACTTGCAGGGGCTTCCCAACCTTACCAGAGGG 2886

Qy 5051 CGCCCAGCTGGCAATTCCGGTTCGCTTGCTGTCCATAAAACCGCCCAGTCAGTTATCG 5110
Db 2885 CGCCCAGCTGGCAATTCCGGTTCGCTTGCTGTCCATAAAACCGCCCAGTCAGTCTATCG 2826

Qy 5111 CCATGTAAGCCCACTGCGAAGCTACCTGCGTTTCTCTTTCGGCGTTCCCTTGTCCA 5170
Db 2825 CCATGTAAGCCCACTGCGAAGCTACCTGCGTTTCTCTTTCGGCGTTCCCTTGTCCA 2766

Qy 5171 GATAGCCCAGTAGCTGACATTCATCCGGGGTCAGCACCGTTTCTGCGGACTGGCTTTCTA 5230
Db 2765 GATAGCCCAGTAGCTGACATTCATCCGGGGTCAGCACCGTTTCTGCGGACTGGCTTTCTA 2706

Qy 5231 CGTG 5234
Db 2705 CGTG 2702
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RESULT 10
AAV33630/c
ID   AAV33630 standard; DNA; 6561 BP.
XX
AC   AAV33630;
XX
DT   29-DEC-1998  (first entry)
XX
DE   Plasmid VLSNO2 DNA sequence used in the method of the invention.
XX
KW   Class IIS restriction endonuclease recognition site; LTR;
KW   endogenous mouse promoter element; tissue-specific gene expression;
KW   hormone-specific gene expression; mouse VL30 genome;
KW   developmental-specific gene expression; long terminal repeat; ss.
XX
OS   Synthetic.
XX
PN   WO9838326-A1.
XX
PI   Hodgson CP, Zink MA, Xu G;
XX
PD   03-SEP-1998.
XX
PF   28-FEB-1998;   98WO-US003918.
XX
PR   28-FEB-1997;   97US-0070910P.
XX
PA   (NATU-) NATURE TECHNOLOGY CORP.
XX
DR   WPI; 1998-495399/42.
XX
PT   Method for assembling gene or gene vector - comprises use of primers
PT   containing class IIS restriction endonuclease recognition sites.
XX
PS   Example 3; Page 110-113; 141pp; English.
XX
CC   The invention provides a novel method for directing self-assembly of a
CC   gene having three or more fragments in a directionally and spatially
CC   ordered fashion to produce a gene or a gene vector. The method involves
CC   usage of primers, containing class IIS restriction endonuclease
CC   recognition sites, for isolation of these fragments. As described in the
CC   disclosure, the method may also use a vector for the incorporation and
CC   screening of endogenous mouse promoter elements for the identification of
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3981  Qy  CTCCAGCATGAGATCCCCGCTGGAGGATCATCCAGCCGGCGTCCCGGAAAACGATTCC     4040
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1674  Db  CTCCAGCATGAGATCCCCGCTGGAGGATCATCCAGCCGGCGTCCCGGAAAACGATTCC     1615

4041  Qy  GAAGCCCAACCTTTCATAGAAGAGGCGGCGGGTGGAATCGAAATCTCGTGATGGCAGGTTGGG  4100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1614  Db  GAAGCCCAACCTTTCATAGAAGAGGCGGCGGGTGGAATCGAAATCTCGTGATGGCAGGTTGGG  1555

4101  Qy  CGTCGCTTGGTGCGGTCATTTGAACCCCAGAGTCCGCTCAGAGAGAACTCGTCAGAAGG     4160
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1554  Db  CGTCGCTTGGTGCGGTCATTTGAACCCCAGAGTCCGCTCAGAGAGAACTCGTCAGAAGG     1495

4161  Qy  CGATAGAAGGCGATGCGCTGCGAATCGGAGGCGCGGATACCGTAAAGCACGAGGAAGCCG    4220
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1494  Db  CGATAGAAGGCGATGCGCTGCGAATCGGAGGCGCGGATACCGTAAAGCACGAGGAAGCCG    1435

4221  Qy  TCAGCCCATTCGCCGCCAAGCTCTTCAGCAATATCACGGGTAGCCAACGCTATGTCCTGA    4280
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1434  Db  TCAGCCCATTCGCCGCCAAGCTCTTCAGCAATATCACGGGTAGCCAACGCTATGTCCTGA    1375

4281  Qy  TAGCGGTCCGCCACACCCAGCCGGCCACAGTCGATGAATCCAGAAAAGCGGCCATTTTCC    4340
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1374  Db  TAGCGGTCCGCCACACCCAGCCGGCCACAGTCGATGAATCCAGAAAAGCGGCCATTTTCC    1315

4341  Qy  ACCATGATATTCGGCAAGCAGCATCGCCATGGTCACGACGAGTCCTCGCCGTCGGGC      4400
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1314  Db  ACCATGATATTCGGCAAGCAGCATCGCCATGGTCACGACGAGTCCTCGCCGTCGGGC      1255

4401  Qy  ATGCGGCGCCTTGAGCCTGGCGAACAGTTCGGCTGGCGCGAGCCCCTGATGCTCTTCGTCC   4460
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1254  Db  ATGCGGCGCCTTGAGCCTGGCGAACAGTTCGGCTGGCGCGAGCCCCTGATGCTCTTCGTCC   1195

4461  Qy  AGATCATCCTGATGACAAGACCGGCTTCCATCCGAGTACGTGCTCGCTCGATGCGATGT    4520
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1194  Db  AGATCATCCTGATGACAAGACCGGCTTCCATCCGAGTACGTGCTCGCTCGATGCGATGT    1135

4521  Qy  TTCGCTTGGTGGTCGAATGGGCAGGTAGCCGGATCAAGCGTATGCAGCCGCCGCATTGCA   4580
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1134  Db  TTCGCTTGGTGGTCGAATGGGCAGGTAGCCGGATCAAGCGTATGCAGCCGCCGCATTGCA   1075

4581  Qy  TCAGCCATGATGATACTTTCTGGCAGGAGCAAGGTGAGATGACAGGAGATCCTGCCCC     4640
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1074  Db  TCAGCCATGATGATACTTTCTGGCAGGAGCAAGGTGAGATGACAGGAGATCCTGCCCC     1015

4641  Qy  GGCACTTCGCCCAATAGCAGCCAGTCCCTTCCCGCTTCAGTGACAACGTCGAGCACAGCT   4700
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1014  Db  GGCACTTCGCCCAATAGCAGCCAGTCCCTTCCCGCTTCAGTGACAACGTCGAGCACAGCT   955

4701  Qy  GCGCAAGGAACGCCCGTCGGTGGCCAGCCACGATAGCCGGCTGCCTCGTCCTGCGAGTTCA  4760
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
954   Db  GCGCAAGGAACGCCCGTCGGTGGCCAGCCACGATAGCCGGCTGCCTCGTCCTGCGAGTTCA  895

4761  Qy  TTCAGGGCACCGACAGGTCGGTCTTTGACAAAAAGAACCGGGGCGCCCCTGCGCTGACAGC  4820
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
894   Db  TTCAGGGCACCGACAGGTCGGTCTTTGACAAAAAGAACCGGGGCGCCCCTGCGCTGACAGC  835

4821  Qy  CGGAACACGGCGGCATCAGAGCAGCCGATTGTCTGTTGTGCCCAGTCATAGCCGAATAGC   4880
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
834   Db  CGGAACACGGCGGCATCAGAGCAGCCGATTGTCTGTTGTGCCCAGTCATAGCCGAATAGC   775

4881  Qy  CTCTCCACCCAAGCGGCCGGAGAACCTGCGTGCAATCCATCTTGTTCAATCATCGGAAAC   4940
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
774   Db  CTCTCCACCCAAGCGGCCGGAGAACCTGCGTGCAATCCATCTTGTTCAATCATCGGAAAC   715

4941  Qy  GATCCTCATCCTGTCTCTTGATCAGATCTTGATCCCCTGCGCCATCAGATCCTTGGCGGC   5000
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
714   Db  GATCCTCATCCTGTCTCTTGATCAGATCTTGATCCCCTGCGCCATCAGATCCTTGGCGGC   655

5001  Qy  AAGAAAGCCATCCAGTTTACTTTGCAGGGCTTCCCAACCTTACCAGAGGGCGCCCCAGCT   5060
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
654   Db  AAGAAAGCCATCCAGTTTACTTTGCAGGGCTTCCCAACCTTACCAGAGGGCGCCCCAGCT   595


5061  Qy  GGCAATTCCGGTTCCTTGCTTGCTGTCCATAAAACCGGCCAGTCTAGCTATCCCATGTAAGC   5120
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
594   Db  GGCAATTCCGGTTCCTTGCTTGCTGTCCATAAAACCGGCCAGTCTAGCTATCCCATGTAAGC   535

5121  Qy  CCACTGCAAGCTACCTGCTTCCTTCGGCTTGCGTTTCCGTTGTTTCCCTTGTCCAGATAGCCCAG  5180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
534   Db  CCACTGCAAGCTACCTGCTTCCTTCGGCTTGCGTTTCCGTTGTTTCCCTTGTCCAGATAGCCCAG  475

5181  Qy  TAGCTGACATTCATCCGGCGGTCAGCAGCGTTCTGCGACTGGCTTTCTACGTGTTCCGC     5240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
474   Db  TAGCTGACATTCATCCGGCGGTCAGCAGCGTTCTGCGACTGGCTTTCTACGTGTTCCGC     415

5241  Qy  TTCCTTTAGCAGCCCTTGCGCCCTGAGTGCTTGCGGCAGCGTG     5283
           |||||||||||||||||||||||||||||||||||||||||||
414   Db  TTCCTTTAGCAGCCCTTGCGCCCTGAGTGCTTGCGGCAGCGTG     372
```

RESULT 11
ABQ78294
ID   ABQ78294 standard; DNA; 2192 BP.
XX
AC   ABQ78294;
XX
DT   05-NOV-2002 (first entry)
XX
DE   Nucleotide sequence of plasmid pVC0289.
XX
KW   Pig; growth hormone releasing hormone; GHRH; growth rate; lean body mass;
KW   Insulin-like Growth Factor-I; IGF-I; milk production; feed efficiency;
KW   somatotroph; growth-related disorder; hypopituitary dwarfism;
KW   meat production; egg production; ss.
XX
OS   Synthetic.
XX
PN   WO200261037-A2.
XX
PD   08-AUG-2002.
XX
PF   12-DEC-2001; 2001WO-US048726.
XX
PR   12-DEC-2000; 2000US-0255021P.
XX
PA   (BAYU) BAYLOR COLLEGE MEDICINE.
PA   (ADVI-) ADVISYS.
XX
PI   Schwartz RJ, Carpenter RH, Draghia-Akli R, Kern DR, Smith RG;
XX
DR   WPI; 2002-619237/66.
XX
PT   Improving or enhancing growth, lean body mass, milk production, feed
PT   efficiency or Insulin-like Growth Factor-I levels, comprises introducing
PT   a vector encoding a growth hormone releasing hormone into an animal
PT   before or during gestation.
XX
PS   Example 2; Page 111-112; 113pp; English.
XX
CC   The present sequence represents plasmid pVC0289, which was used to create
CC   a vector carrying cDNA encoding pig growth hormone releasing hormone
CC   (GHRH) cDNA. Nucleic acids encoding GHRH are used in the method of the
CC   invention. The specification describes a method for improving or
CC   enhancing characteristics e.g. growth, lean body mass, Insulin-like
CC   Growth Factor (IGF)-I levels, growth rate and milk production in an
CC   offspring, and for delaying birth of an offspring. The method comprises
CC   introducing a vector, encoding GHRH, into cells of the female animal
CC   prior to or during gestation of the offspring under conditions where the
CC   nucleotide sequence is expressed. The method is useful of improving or
CC   enhancing animal growth, for increasing growth hormone, lean body mass,
CC   IGF-I levels, feed efficiency, growth rate, ratio of somatotrophs to
CC   other hormone-producing cells in a pituitary gland, and milk production
CC   in an offspring, and for delaying birth of an offspring. GHRH nucleic
CC   acids and vectors are used for diagnostic purposes in clinical medicine,
CC   both human and veterinary, e.g. in treating growth-related disorders such
CC   as hypopituitary dwarfism resulting from abnormalities in growth hormone

```
CC   production, and in stimulating the growth and enhancing feed conversion
CC   efficiency of animals raised for meat, milk and egg production
XX
SQ   Sequence 2192 BP; 486 A; 634 C; 601 G; 471 T; 0 U; 0 Other;

Query Match       30.4%;   Score 1603.8; DB 6; Length 2192;
Best Local Similarity   82.8%;   Pred. No. 2.6e-234;
Matches 2022;   Mismatches   0;   Conservative   0;   Indels   392;   Gaps   1;
```

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Qy  2706 CTAGACGTAATCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCC 2765
         ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    70 CTTGGCCTAATCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCC  129

Qy  2766 ACACAACATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTA 2825
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   130 ACACAACATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTA  189

Qy  2826 ACTCACATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCA 2885
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   190 ACTCACATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCA  249

Qy  2886 GCTGCATTAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTC 2945
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   250 GCTGCATTAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTC  309

Qy  2946 CGCTTCCTCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGC 3005
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   310 CGCTTCCTCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGC  369

Qy  3006 TCACTCAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACAT 3065
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   370 TCACTCAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACAT  429

Qy  3066 GTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTT 3125
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   430 GTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTT  489

Qy  3126 CCATAGGCTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCG 3185
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   490 CCATAGGCTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCG  549

Qy  3186 AAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTC 3245
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   550 AAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTC  609

Qy  3246 TCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGT 3305
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   610 TCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGT  669

Qy  3306 GGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAA 3365
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   670 GGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAA  729

Qy  3366 GCTGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTA 3425
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   730 GCTGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTA  789

Qy  3426 TCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAA 3485
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   790 TCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAA  849

Qy  3486 CAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAA 3545
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   850 CAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAA  909

Qy  3546 CTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTT 3605
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   910 CTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTT  969

Qy  3606 CGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTT 3665
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   970 CGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTT 1029
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Qy  3666 TTTTGTTTGCAAGCAGCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGAT 3725
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1030 TTTTGTTTGCAAGCAGCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGAT 1089

Qy  3726 CTTTTCTACGGGGTCTGACGCTCAGTGGAACGAAAACTCACGTTAAGGGATTTTGGTCAT 3785
         ||||||||||||||||||
Db  1090 CTTTTCTACGGGGTCTGA----------------------------------------- 1107

Qy  3786 GAGATTATCGTCGACCAAAGCGCCATCGTGCTCCCCACTCCTGCCTCCCCACTCCTGCCATG 3845
Db  1108 ------------------------------------------------------------ 1107

Qy  3846 GATGCGCGGATAGCCGCTGCTCGTTTCCTGATGCCGCACGGATTTGACTGCCGGTAGAA 3905
Db  1108 ------------------------------------------------------------ 1107

Qy  3906 CTCCGCGGAGGTCGTCAGCCTTCAGGCAGCAGCTGACCAACTCGCGAGGGGATCGAGCCC 3965
Db  1108 ------------------------------------------------------------ 1107

Qy  3966 GGGGTGGGGCGAAGAACTCCAGCATGAGATCCCCGCTGGAGGATCATCCAGCCGCGGCGTC 4025
Db  1108 ------------------------------------------------------------ 1107

Qy  4026 CCGGAAAACGATTCCGAAGCCCAACCTTTCATAGAAGGCGGCGGTGGAATCGAAAATCTCG 4085
Db  1108 ------------------------------------------------------------ 1107

Qy  4086 TGATGGCAGGTTGGGGTGCGCTTGGTCGGTCATTCGAACCCGAGAGTCCCGCTCAGAAG 4145
                                                         ||||||||||
Db  1108 -------------------------------------------------CGCTCAGAAG 1117

Qy  4146 AACTCGTCAAGAAGGCGATAGAAGGCGATGGGGACGGCTGGAATCGGGACGGCGATACCGTAA 4205
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1118 AACTCGTCAAGAAGGCGATAGAAGGCGATGGGGACGGCTGGAATCGGGACGGCGATACCGTAA 1177

Qy  4206 AGCACGAGGAGCGGTCAGCCCATTCGCCGCCAAGCTCTTCAGCAATATCACGGGTAGCC 4265
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1178 AGCACGAGGAGCGGTCAGCCCATTCGCCGCCAAGCTCTTCAGCAATATCACGGGTAGCC 1237

Qy  4266 AACGCTATGTCCTGATAGCGGTCCGCCACACCCAGCCGGCCACAGTCGATGAATCCAGAA 4325
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1238 AACGCTATGTCCTGATAGCGGTCCGCCACACCCAGCCGGCCACAGTCGATGAATCCAGAA 1297

Qy  4326 AAGCGGCCATTTTCCACCATGATATTCGGCAAGCAGGCATCGCCATGGGTCACGACGAGA 4385
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1298 AAGCGGCCATTTTCCACCATGATATTCGGCAAGCAGGCATCGCCATGGGTCACGACGAGA 1357

Qy  4386 TCCTCGCCGTCGGGCATGCGCGCCTTGAGCCTGGCGAACAGTTCGGCTGGCGCGAGCCCC 4445
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1358 TCCTCGCCGTCGGGCATGCGCGCCTTGAGCCTGGCGAACAGTTCGGCTGGCGCGAGCCCC 1417

Qy  4446 TGATGCTCTTCGTCCAGATCATCCTGATCGACAAGACCGGCTTCCATCCGAGTACGTGCT 4505
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1418 TGATGCTCTTCGTCCAGATCATCCTGATCGACAAGACCGGCTTCCATCCGAGTACGTGCT 1477

Qy  4506 CGCTCGATGGCGATGTTTCGCTTGGTGGTCGAATGGGCAGGTAGCCGGATCAAGCGTATGC 4565
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1478 CGCTCGATGGCGATGTTTCGCTTGGTGGTCGAATGGGCAGGTAGCCGGATCAAGCGTATGC 1537

Qy  4566 AGCCGCCGCATTCGCATCAGCCATGATGGATACTTTCTCGGCAGGAGCAAGGTGAGATGAC 4625
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1538 AGCCGCCGCATTCGCATCAGCCATGATGGATACTTTCTCGGCAGGAGCAAGGTGAGATGAC 1597

Qy  4626 AGGAGATCGCTGCCCCGGCACTTCGCCCAATAGCAGCCAGTCCCTTCCCGGCTTCAGTGACA 4685
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1598 AGGAGATCGCTGCCCCGGCACTTCGCCCAATAGCAGCCAGTCCCTTCCCGGCTTCAGTGACA 1657

Qy  4686 ACGTCGAGCACAGCTGCGCAAGGAACGCCCGTCGTGGCCAGCCACGATAGCCGCGCTGCC 4745
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1658 ACGTCGAGCACAGCTGCGCAAGGAACGCCCGTCGTGGCCAGCCACGATAGCCGCGCTGCC 1717

Qy  4746 TCGTCCTGCAGTTCATTCAGGGCACCGGACAGGTCGGTCTTGACAAAAAGAACCGGGCGC 4805
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delaying birth of an offspring. The method comprises introducing a
vector, encoding GHRH, into cells of the female animal prior to or during
gestation of the offspring under conditions where the nucleotide sequence
is expressed. The method is useful of improving or enhancing animal
growth, for increasing growth hormone, lean body mass, IGF-I levels, feed
efficiency, growth rate, ratio of somatotrophs to other hormone-producing
cells in a pituitary gland, and milk production in an offspring, and for
delaying birth of an offspring. GHRH nucleic acids and vectors are used
for diagnostic purposes in clinical medicine, both human and veterinary,
e.g. in treating growth-related disorders such as hypopituitary dwarfism
resulting from abnormalities in growth hormone production, and in
stimulating the growth and enhancing feed conversion efficiency of
animals raised for meat, milk and egg production

XX
SQ   Sequence 3534 BP; 764 A; 1018 C; 979 G; 773 T; 0 U; 0 Other;

Query Match   30.4%;   Score 1603.8; DB 6;   Length 3534;
Best Local Similarity   82.8%;   Pred. No. 2.5e-234;
Matches 2022;   Conservative   0;   Mismatches   27;   Indels   392;   Gaps   1;

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Qy  2706 CTAGACGTAATCATGTCATAGCTGTTCCTGTGTGAAATTGTATCCGCTCACAATTCC 2765
         ||||| ||||||||||||||||||||  |||||||||||||||||||||||||||||
Db  1412 CTTGGCGTAATCATGTCATAGCTGTTTCCTGTGTGAAATTGTATCCGCTCACAATTCC 1471

Qy  2766 ACACAACATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCTAATGAGTGAGCTA 2825
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1472 ACACAACATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCTAATGAGTGAGCTA 1531

Qy  2826 ACTCACATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCA 2885
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1532 ACTCACATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCA 1591

Qy  2886 GCTGCATTAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTC 2945
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1592 GCTGCATTAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTC 1651

Qy  2946 CGCTTCCTCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGC 3005
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1652 CGCTTCCTCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGC 1711

Qy  3006 TCACTCAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACAT 3065
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1712 TCACTCAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACAT 1771

Qy  3066 GTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTT 3125
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1772 GTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTT 1831

Qy  3126 CCATAGGCTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCG 3185
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1832 CCATAGGCTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCG 1891

Qy  3186 AAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTC 3245
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1892 AAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTC 1951

Qy  3246 TCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGT 3305
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1952 TCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGT 2011

Qy  3306 GGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAA 3365
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2012 GGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAA 2071

Qy  3366 GCTGGGCTGTGTGCACGAACCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTA 3425
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2072 GCTGGGCTGTGTGCACGAACCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTA 2131

Qy  3426 TCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAA 3485
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2132 TCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAA 2191

Qy  3486 CAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAA 3545
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Db  1718 TCGTCCTCGCAGTTCATTCAGGGCACCGGACCAGGTCGGTCTTGACAAAAGAACCGGGCGC 1777

Qy  4806 CCCTGCGCTGACAGCGGGAACACCGGCATCAGAGCAGCGGATTGTCGTTGTGCCCAG 4865
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1778 CCCTGCGCTGACAGCGGGAACACCGGCATCAGAGCAGCGGATTGTCGTTGTGCCCAG 1837

Qy  4866 TCATAGCCGAATAGCCTCTCCACCCAAGCGGCCGGAGAACCTGCGTGCAATCATCTTGT 4925
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1838 TCATAGCCGAATAGCCTCTCCACCCAAGCGGCCGGAGAACCTGCGTGCAATCCATCTTGT 1897

Qy  4926 TCAATCATGCGAAACGATCCTCATCCTGTCTCTTGATCAGATCTTGATCCCCTGCGCCAT 4985
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1898 TCAATCATGCGAAACGATCCTCATCCTGTCTCTTGATCAGATCTTGATCCCCTGCGCCAT 1957

Qy  4986 CAGATCCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTGCAGGGCTTCCCAACCTTACCA 5045
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1958 CAGATCCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTGCAGGGCTTCCCAACCTTACCA 2017

Qy  5046 GAGGGCGCCCCAGCTGGCAATTCCGGTTCGCTTGCTGTCCATAAAACCGCCCAGTCTAGC 5105
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2018 GAGGGCGCCCCAGCTGGCAATTCCGGTTCGCTTGCTGTCCATAAAACCGCCCAGTCTAGC 2077

Qy  5106 TATCGCCATGTAAGCCACTGCAAGCTACCTGCTTTCTCTT 5146
         ||||||| |||| ||  |||  |  ||
Db  2078 AACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGCTATT 2118
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RESULT 12
ABQ78293
ID   ABQ78293 standard; DNA; 3534 BP.
XX
AC   ABQ78293;
XX
DT   05-NOV-2002 (first entry)
XX
DE   Nucleotide sequence of vector pSPc5-12-HV-GHRH.
XX
KW   Pig; growth hormone releasing hormone; GHRH; growth rate; lean body mass;
KW   Insulin-like Growth Factor-I; IGF-I; milk production; feed efficiency;
KW   somatotroph; growth-related disorder; hypopituitary dwarfism;
KW   meat production; egg production; ss.
XX
OS   Synthetic.
XX
PN   WO200261037-A2.
XX
PD   08-AUG-2002.
XX
PF   12-DEC-2001; 2001WO-US048726.
XX
PR   12-DEC-2000; 2000US-0255021P.
XX
PA   (BAYU) BAYLOR COLLEGE MEDICINE.
PA   (ADVI-) ADVISYS.
XX
PI   Schwartz RJ, Carpenter RH, Draghia-Akli R, Kern DR, Smith RG;
XX
DR   WPI; 2002-619237/66.
XX
PT   Improving or enhancing growth, lean body mass, milk production, feed
PT   efficiency or Insulin-like Growth Factor-I levels, comprises introducing
PT   a vector encoding a growth hormone releasing hormone into an animal
PT   before or during gestation.
XX
PS   Example 2; Page 109-111; 113pp; English.
XX
CC   The present sequence represents vector pSPc5-12-HV-GHRH, which carries
CC   cDNA encoding pig growth hormone releasing hormone (GHRH) cDNA. Nucleic
CC   acids encoding GHRH are used in the method of the invention. The
CC   specification describes a method for improving or enhancing
CC   characteristics e.g. growth, lean body mass, Insulin-like Growth Factor
CC   (IGF)-I levels, growth rate and milk production in an offspring, and for

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Db   2192 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| 
          CAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAAGTTCTTGAAGTGGTGGCCTAA 2251

Qy   3546 CTACGGCTACACTAGAAGAACAGTATTTGGTATCGCGGCTCTGAAGCCAGTTACCTT 3605
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2252 CTACGGCTACACTAGAAGAACAGTATTTGGTATCGCGGCTCTGAAGCCAGTTACCTT 2311

Qy   3606 CGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAACAACCACCGGTAGGCGGTGGTTT 3665
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2312 CGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAACAACCACCGCTGGTAGGCGGTGGTTT 2371

Qy   3666 TTTTGTTTGCAAGCAGCAGATTACGGCGAGAAAAAAAGGATCTCAAGAAGATCCTTTGAT 3725
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2372 TTTTGTTTGCAAGCAGCAGATTACGGCGAGAAAAAAAGGATCTCAAGAAGATCCTTTGAT 2431

Qy   3726 CTTTTCTACGGGGTCTGACGCTCAGTGGAACGAAAACTCACGTTAAGGGATTTTGGTCAT 3785
          ||||||||||||||||| ----- 
Db   2432 CTTTTCTACGGGGTCTGA----------------- 2449

Qy   3786 GAGATTATCGTCGACCAAAGCGGCCATCGTGCCTCCCCACTCGTGCAGTTCGGGGGCATG 3845
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db                  --------------------- 2449

Qy   3846 GATGCGCGGATAGCCGCTGCTGTTTCCTGGATGCCCACGGAGATTTGCACTGCCGTAGAA 3905
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db                  --------------------- 2449

Qy   3906 CTCCGCGGAGGTCGTCCCAGGCAGCAGCCTCGAACCAACTCGCCGAGGGGGATCGAGCCC 3965
          ----------------------
Db                  --------------------- 2449

Qy   3966 GGGGTGGGCGGAAGAACTCCAGCATGAGATCCCCGCCGTTGGACGAGGATCATCCAGCCGCGTC 4025
          ----------------------
Db                  --------------------- 2449

Qy   4026 CCGGAAAAACGATTCCGAAGCCCAAACCTTTCATAGAAGAGGCGGGCGGTGGAAATCGAAATCTCG 4085
          ----------------------
Db                  --------------------- 2449

Qy   4086 TGATGGCAGGTTGGGCGGTCGCGTTGGTCGGTCATTTCGAACCCCAGAGTCCCGCTCAGAAG 4145
                                              ||||||||
Db                              --------CGCTCAGAAG 2459

Qy   4146 AACTCGTCAAGAAGGCGATAGAGGCGATGCGCTGGCGAATCGGAGAGGCGGCGATACCGTAA 4205
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2460 AACTCGTCAAGAAGGCGATAGAGGCGATGCGCTGGCGAATCGGAGAGGCGGCGATACCGTAA 2519

Qy   4206 AGCACGAGGAAGGCGGTCAGCCCATTGCGCGCCAAGCTCTTCAGCAATATCACGGGTAGCC 4265
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2520 AGCACGAGGAAGGCGGTCAGCCCATTGCGCGCCAAGCTCTTCAGCAATATCACGGGTAGCC 2579

Qy   4266 AACGCTATGTCCTGATAGCGGTCCGCCACACCCAGCCGGCCACAGTCGATGAATCCAGAA 4325
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2580 AACGCTATGTCCTGATAGCGGTCCGCCACACCCAGCCGGCCACAGTCGATGAATCCAGAA 2639

Qy   4326 AAGCGGCCATTTTCCACCATGATATTCGGCAAGCAGGCATGCCATGGTCACGACGAGA 4385
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2640 AAGCGGCCATTTTCCACCATGATATTCGGCAAGCAGGCATGCCCATGGTCACGACGAGA 2699

Qy   4386 TCCTCGCCGTCGGGCATGCGCGCCTTGAGCCTGGCGAACAGTTCGGCTGGCGCGAGCCCC 4445
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2700 TCCTCGCCGTCGGGCATGCGCGCCTTGAGCCTGGCGAACAGTTCGGCTGGCGCGAGCCCC 2759

Qy   4446 TGATGCTCTTCGTCCAGATCATCCTGATGACAAGACCGGCTTCATCCGAGTACGTGCT 4505
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2760 TGATGCTCTTCGTCCAGATCATCCTGATGACAAGACCGGCTTCATCCGAGTACGTGCT 2819

Qy   4506 CGCTCGATGCGATGTTTCGCTTGGTCGTGGTCGGATCGCAGGTAGCCCGGATCAAGCGTATGC 4565
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2820 CGCTCGATGCGATGTTTCGCTTGGTCGTGGTCGGATGGGCAGGTAGCCCGGATCAAGCGTATGC 2879

Qy   4566 AGCCGCCGCATTGCATCAGCCATGATGGATACTTTCTCGGCAGGAGCAAGGTGAGATGAC 4625
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db   2880 AGCCGCCGCATTGCATCAGCCATGATGGATACTTTCTCGGCAGGAGCAAGGTGAGATGAC 2939

Qy   4626 AGGAGATCCTGCCCCGGCACTTCGCCCAATAGCAGCCAGTCCCTTCCCGCTTCCAGTGACA 4685
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2940 AGGAGATCCTGCCCCGGCACTTCGCCCAATAGCAGCCAGTCCCTTCCCGCTTCCCAGTGACA 2999

Qy   4686 ACGTCGAGCACAGCTGCCGAAGGAACGCCCGTCGTGGCCAGCCACGATAGCCGCGCTGCC 4745
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3000 ACGTCGAGCACAGCTGCCGAAGGAACGCCCGTCGTGGCCAGCCACGATAGCCGCGCTGCC 3059

Qy   4746 TCGTCCTGCAGTTCATTCAGGGCACCGGACAGGTCGGTCTTGACAAAAGAACCGGGCGC 4805
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3060 TCGTCCTGCAGTTCATTCAGGGCACCGGACAGGTCGGTCTTGACAAAAGAACCGGGCGC 3119

Qy   4806 CCCTGCGCTGACGCCGGAACACGGGCGGCATCAGAGCGGCGATTGTCTGTTGTGCCCAG 4865
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3120 CCCTGCGCTGACGCCGGAACACGGGCGGCATCAGAGCGGCGATTGTCTGTTGTGCCCAG 3179

Qy   4866 TCATAGCCGAATAGCCTCTCCACCCAAGCGGCCGGAGAACCTGCGTGCAATCATCTTGT 4925
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3180 TCATAGCCGAATAGCCTCTCCACCCAAGCGGCCGGAGAACCTGCGTGCAATCATCTTGT 3239

Qy   4926 TCAATCATGCGAAACGATCCTCGTCTCTTGATCAGATCTTGATCCCCTGCGCCAT 4985
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3240 TCAATCATGCGAAACGATCCTCGTCTCTTGATCAGATCTTGATCCCCTGCGCCAT 3299

Qy   4986 CAGATCCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTGCAGGGCTTCCAACCTTACCA 5045
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3300 CAGATCCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTGCAGGGCTTCCAACCTTACCA 3359

Qy   5046 GAGGGCGCCCAGCTGGCAATTCCGGTTCGCTTGCTGTCGTCCATAAAACCCCAGTCTAGC 5105
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3360 GAGGGCGCCCAGCTGGCAATTCCGGTTCGCTTGCTGTCGTCCATAAAACCCCAGTCTAGC 3419

Qy   5106 TATCGCCATGTAAGCCCACTGCGAAGCTACCTGCTTTCTCTT 5146
          ||||||||||||||||||||||||||||||||||||
Db   3420 AACTGTTGGAAGGGCGATCGGTGCGGGCCTCTTCGCTATT 3460
```

RESULT 13
AAL62060
ID   AAL62060 standard; DNA; 3534 BP.
XX
AC   AAL62060;
XX
DT   22-SEP-2003 (first entry)
XX
DE   TV-GHRH plasmid DNA.
XX
KW   Plasmid-mediated supplementation; anaemia; tumour; adenoma; melanoma;
KW   sarcoma; immune dysfunction; carcinoma; leukaemia; kidney failure;
KW   lymphoma; weight loss; lymphopoesis; appetite stimulant; anoretic;
KW   growth hormone releasing hormone; GHRH; cyclic; circular; gene; ds.
XX
OS   Unidentified.
XX
PN   WO200349700-A2.
XX
PD   19-JUN-2003.
XX
PF   10-DEC-2002; 2002WO-US039509.
PR   11-DEC-2001; 2001US-0339610P.
XX
PA   (ADVI-) ADVISYS INC.
PA   (BAYU) BAYLOR COLLEGE MEDICINE.
XX
PI   Draghia-Akli R, Carpenter RH, Kern DR, Schwartz RJ, King G;
PI   Hahn K, Brenner MK;
XX
DR   WPI; 2003-558968/52.
XX
PT   Treating anemia, immune dysfunction, tumor, increasing total red blood

PT cell mass, reversing wasting or abnormal weight loss in subject, by
PT administering nucleic acid construct encoding growth-hormone-releasing-
PT hormone.
XX
PS Claim 4; Page 193-195; 212pp; English.
XX
CC The invention relates to compositions and methods for plasmid-mediated
CC supplementation. The method is useful for treating anaemia, tumour (such
CC as adenoma, mast cell tumour, melanoma, sarcoma or solid tumour), immune
CC dysfunction, carcinoma (benign or malignant), leukaemia, lymphoma or
CC kidney failure, for preventing the development of metastatic tumour, for
CC increasing total red blood cell mass, for reversing wasting, abnormal
CC weight loss or suppression of lymphopoesis, in a subject, or for
CC increasing weight gain in a chronically ill subject or, or for extending
CC life expectancy for a chronically ill subject. The present sequence is TV
CC -growth hormone releasing hormone (GHRH) plasmid DNA. This sequence is
CC used to illustrate the method of the invention
XX
SQ Sequence 3534 BP; 764 A; 1016 C; 979 G; 775 T; 0 U; 0 Other;

Query Match   30.4%; Score 1603.8; DB 9; Length 3534;
Best Local Similarity 82.8%; Pred. No. 2.5e-234;
Matches 2022; Conservative 0; Mismatches 27; Indels 392; Gaps 1;

Qy   2706 CTAGACGTAATCATGTCATAGCTGTTCCTGTGTGAAATTGTTATCCGCTCACAATTCC 2765
          ||||||||||||||||||||||| |||||||| ||||||||||||||||||||||||||
Db   1412 CTTGGCGTAATCATGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCC 1471

Qy   2766 ACACAACATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTA 2825
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1472 ACACAACATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTA 1531

Qy   2826 ACTCACATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCA 2885
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1532 ACTCACATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCA 1591

Qy   2886 GCTGCATTAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTC 2945
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1592 GCTGCATTAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTC 1651

Qy   2946 CGCTTCCTCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGC 3005
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1652 CGCTTCCTCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGC 1711

Qy   3006 TCACTCAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACAT 3065
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1712 TCACTCAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACAT 1771

Qy   3066 GTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTT 3125
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1772 GTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTT 1831

Qy   3126 CCATAGGCTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCG 3185
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1832 CCATAGGCTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCG 1891

Qy   3186 AAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTC 3245
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1892 AAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTC 1951

Qy   3246 TCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGT 3305
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1952 TCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGT 2011

Qy   3306 GGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAA 3365
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2012 GGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAA 2071

Qy   3366 GCTGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTA 3425
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2072 GCTGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTA 2131

Qy   3426 TCGTCTTGAGTCCAACCCGGTAAGACAGACGACTTATCGCCACTGGCAGCAGCCACTGTAA 3485
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2132 TCGTCTTGAGTCCAACCCGGTAAGACAGACGACTTATCGCCACTGGCAGCAGCCACTGTAA 2191

Db   3486 CAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGCCTAA 3545
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   2192 CAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGCCTAA 2251

Qy   3546 CTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTT 3605
          |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db   2252 CTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTT 2311

Qy   3606 CGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTT 3665
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2312 CGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTT 2371

Qy   3666 TTTTGTTGCAAGCAGCAGATTACGGCGCAGAAAAAAAGGATCCAAGATCTCCTTTGAT 3725
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2372 TTTTGTTGCAAGCAGCAGATTACGGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGAT 2431

Qy   3726 CTTTTCTACGGGGTCTGACGCTCAGTGGAACGAAAACTCACGTTAAGGGATTTTGGTCAT 3785
          |||||||||||||||||
Db   2432 CTTTTCTACGGGGTCTGA------------------- 2449

Qy   3786 GAGATTATCGTCGACCAAAGCCGCCATCGTGCCCTCCCACTCCTGCCCTCCGGGGCATG 3845

Db   2450 ------------- 2449

Qy   3846 GATGCGCGGATAGCCGCTGCTGGTTTCCTGGATGCCGCAGACGGATTTGCACTGCCGGTAGAA 3905

Db   2450 ----------------- 2449

Qy   3906 CTTCCGCGGAGGTCGTCCAGCCTTCAGGCAGCAGCAGCTGAACCAACTCGCGAGGGGATCGAGCCC 3965

Db   2450 --------------- 2449

Qy   3966 GGGGTGGGCGGAAGAACTTCCAGCATGAGCATCATCCAGCCGGCCGGCGTC 4025

Db   2450 --------------- 2449

Qy   4026 CCGGAAAACGATTCCGAAGCCCAACCTTTCATAGAAGGCGGCGTGGAATCGAAAATCTCG 4085

Db   2450 -------------- 2449

Qy   4086 TGATGGCAGGTTGGGCGTCGCTTGGTCGTCATTTCGAACCCCAGAGTCCCGCTCAGAAG 4145

Db   2450 -------CGCTCAGAAG 2459

Qy   4146 AACTCGTCAAGAAGGCGATAGAAGGCGATGCGCTGCGAATCGGGAGGGCGGATACCGTAA 4205
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2460 AACTCGTCAAGAAGGCGATAGAAGGCGATGCGCTGCGAATCGGGAGGGCGGATACCGTAA 2519

Qy   4206 AGCACGAGGAAGCGGTCAGCCCATTCGCCGCCAAGCTCTTCAGCAATATCACGGGTAGCC 4265
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2520 AGCACGAGGAAGCGGTCAGCCCATTCGCCGCCAAGCTCTTCAGCAATATCACGGGTAGCC 2579

Qy   4266 AACGCTATGTCCTGATAGCGGTCCGCCACACCCAGCCGGCCACAGTCGATGAATCCAGAA 4325
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2580 AACGCTATGTCCTGATAGCGGTCCGCCACACCCAGCCGGCCACAGTCGATGAATCCAGAA 2639

Qy   4326 AAGCGGCCATTTTCCACCATGATATTCGGCAAGCAGGCATCGCCATGGGTCACGACGAGA 4385
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2640 AAGCGGCCATTTTCCACCATGATATTCGGCAAGCAGGCATCGCCATGGGTCACGACGAGA 2699

Qy   4386 TCCTCGCCGTCGGGCATGCGCGCCTTGAGCCTGGCGAACAGTTCGGCTGGCGCGAGCCCC 4445
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2700 TCCTCGCCGTCGGGCATGCGCGCCTTGAGCCTGGCGAACAGTTCGGCTGGCGCGAGCCCC 2759

Qy   4446 TGATGCTCTTCGTCCAGATCATCCGCGATCCAGATCATCCGCGATCGACAAGACCGGCTTCCATCCGAGTACGTGCT 4505
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2760 TGATGCTCTTCGTCCAGATCATCCGCGATCGACAAGACCGGCTTCCATCCGAGTACGTGCT 2819

Qy   4506 CGCTCGATGGCGATGTTTCGCTTGGTGGTCGAATGGGCAGGTAGCCGGATCAAGCGTATGC 4565
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3486 CGCTCGATGGCGATGTTTCGCTTGGTGGTCGAATGGGCAGGTAGCCGGATCAAGCGTATGC 3485

```
XX
DR   WPI; 2003-558968/52.
XX
PT   Treating anemia, immune dysfunction, tumor, increasing total red blood
PT   cell mass, reversing wasting or abnormal weight loss in subject, by
PT   administering nucleic acid construct encoding growth-hormone-releasing-
PT   hormone.
XX
PS   Example 1; Page 198-200; 212pp; English.
XX
CC   The invention relates to compositions and methods for plasmid-mediated
CC   supplementation. The method is useful for treating anaemia, tumour (such
CC   as adenoma, mast cell tumour, melanoma, sarcoma or solid tumour), immune
CC   dysfunction, carcinoma (benign or malignant), leukaemia, lymphoma or
CC   kidney failure, for preventing the development of metastatic tumour, for
CC   increasing total red blood cell mass, for reversing wasting, abnormal
CC   weight loss or suppression of lymphopoesis, in a subject, or for
CC   increasing weight gain in a chronically ill subject, or or for extending
CC   life expectancy for a chronically ill subject. The present sequence is
CC   wild-type growth hormone releasing hormone (GHRH) plasmid DNA. This
CC   sequence is used to illustrate the method of the invention
XX
SQ   Sequence 3534 BP; 764 A; 1015 C; 981 G; 774 T; 0 U; 0 Other;

Query Match             30.4%;  Score 1603.8;  DB 9;  Length 3534;
Best Local Similarity   82.8%;  Pred. No. 2.5e-234;
Matches 2022;  Conservative   0;  Mismatches  27;  Indels 392;  Gaps   1;

Qy   2706 CTAGACGTAATCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCC 2765
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1412 CTTGGGCGTAATCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCC 1471

Qy   2766 ACACAACATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTA 2825
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1472 ACACAACATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTA 1531

Qy   2826 ACTCACATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCA 2885
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1532 ACTCACATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCA 1591

Qy   2886 GCTGCATTAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTC 2945
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1592 GCTGCATTAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTC 1651

Qy   2946 CGCTTCCTCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGC 3005
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1652 CGCTTCCTCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGC 1711

Qy   3006 TCACTCAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACAT 3065
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1712 TCACTCAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACAT 1771

Qy   3066 GTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTT 3125
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1772 GTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTT 1831

Qy   3126 CCATAGGCTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCG 3185
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1832 CCATAGGCTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCG 1891

Qy   3186 AAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTC 3245
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1892 AAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTC 1951

Qy   3246 TCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGT 3305
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1952 TCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGT 2011

Qy   3306 GGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAA 3365
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2012 GGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAA 2071

Qy   3366 GCTGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTA 3425
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Db   2820 CGCTCGATGCGATGTTTCGCTGGTGGTCGAATGGGCAGGTAGCCGGATCAAGCGTATGC 2879
Qy   4566 AGCCGCCGATTGCATCAGCCATGATGGATACTTTCTCGGCAGGAGCAAGGTGAGATGAC 4625
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2880 AGCCGCCGCATTGCATCAGCCATGATGGATACTTTCTCGGCAGGAGCAAGGTGAGATGAC 2939

Qy   4626 AGGAGATCCTGCCCCGGACTTCGCCCAATAGCAGCCAGTCCCTTCCCGCTTCAGTGACA 4685
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2940 AGGAGATCCTGCCCCGGACTTCGCCCAATAGCAGCCAGTCCCTTCCCGCTTCAGTGACA 2999

Qy   4686 ACGTCGAGCACAGCTGCCCAAGGAACCGCCGTCGTGCCAGCCACGATAGCCGCTGCC 4745
          ||||  |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3000 ACGTCGAGCACAGCTGCGCGAAGGAACCGCCGTCGTGCCAGCCACGATAGCCGCTGCC 3059

Qy   4746 TCGTCCTGCAGTTCATTCAGGGACACCGGACAGTCGGTCTTGACAAAAGAACCGGGCGC 4805
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3060 TCGTCCTGCAGTTCATTCAGGGACACCGGACAGTCGGTCTTGACAAAAGAACCGGGCGC 3119

Qy   4806 CCCTGGCCTGACAGCCGGAACAGCGGCCGGCATCAGAGCAGCCGATTGTCTGTTGTGCCCAG 4865
          ||||||| |||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db   3120 CCCTGGCGTGACAGCCGGAACACGCGGCCGGCATCAGAGCAGCCGATTGTCTGTTGTGCCCAG 3179

Qy   4866 TCATAGCCGAATAGCCTCTCCACCCAAGCGGCCGGAGAACCTGCGTGCAATCCATCTTGT 4925
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3180 TCATAGCCGAATAGCCTCTCCACCCAAGCGGCCGGAGAACCTGCGTGCAATCCATCTTGT 3239

Qy   4926 TCAATCATGCGAAACGATCCTCATCCTGTCTCTTGATCAGATCTTGATCCCCTGCGCCAT 4985
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3240 TCAATCATGCGAAACGATCCTCATCCTGTCTCTTGATCAGATCTTGATCCCCTGCGCCAT 3299

Qy   4986 CAGATCCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTGCAGGGCTTCCCAACCTTACCA 5045
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3300 CAGATCCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTGCAGGGCTTCCCAACCTTACCA 3359

Qy   5046 GAGGGCGCCCCAGCTGGCAATTCCGGTTCGCTTGCTGTCCATAAAACCGCCCAGTCTAGC 5105
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3360 GAGGGCGCCCCAGCTGGCAATTCCGGTTCGCTTGCTGTCCATAAAACCGCCCAGTCTAGC 3419

Qy   5106 TATCGCCATGTAAGCCCACTGCAAGCTACCTGCTTTCTCTT 5146
              |  |  |||||     ||      |||||||||||
Db   3420 AACTGTGTGGGGAAGGGCGATCCGTGCGGCCCTTCGCTATT 3460
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RESULT 14
AAL62062
ID   AAL62062 standard; DNA; 3534 BP.
XX
AC   AAL62062;
XX
DT   22-SEP-2003 (first entry)
XX
DE   Wild-type GHRH plasmid DNA, pSP-wt-GHRH.
XX
KW   Plasmid-mediated supplementation; anaemia; tumour; adenoma; melanoma;
KW   sarcoma; immune dysfunction; carcinoma; leukaemia; kidney failure;
KW   lymphoma; weight loss; lymphopoesis; appetite stimulant; anoretic;
KW   growth hormone releasing hormone; GHRH; cyclic; circular; gene; ds.
XX
OS   Unidentified.
XX
PN   WO2003049700-A2.
XX
PD   19-JUN-2003.
XX
PF   10-DEC-2002; 2002WO-US039509.
XX
PR   11-DEC-2001; 2001US-0339610P.
XX
PA   (ADVI-) ADVISYS INC.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
XX
PI   Draghia-Akli R, Carpenter RH, Kern DR, Schwartz RJ, King G;
PI   Hahn K, Brenner MK;
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Db   2072 |||||||||||||||||||||||||||||||||||||||||||||||||||||
           GCTGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTA 2131

Qy   3426 TCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCCACTGGTAA 3485
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2132 TCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCCACTGGTAA 2191

Qy   3486 CAGGATTAGCAGAGAGCCAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAA 3545
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2192 CAGGATTAGCAGAGAGCCAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAA 2251

Qy   3546 CTACGGCTACACTAGAAGAACACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTT 3605
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2252 CTACGGCTACACTAGAAGAACACAGTATTTGGTATCTCGCGTCTGCTGAAGCCAGTTACCTT 2311

Qy   3606 CGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAACCACCGCTGGTAGCGGTGGTTT 3665
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2312 CGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAACCACCGCTGGTAGCGGTGGTTT 2371

Qy   3666 TTTTGTTTGCAAGCAGCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGAT 3725
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2372 TTTTGTTTGCAAGCAGCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGAT 2431

Qy   3726 CTTTTCTACGGGGTCTGACGCTCAGTGGAACGAAAACTCACGTTAAGGGATTTTGGTCAT 3785
           ||||||||||||
Db   2432 CTTTTCTACGGGGTCTGA- 2449

Qy   3786 GAGATTATCGTGCGACCAAAGCGGCCCATCGTGCTCCCCACTCCTCGAGTTCGGGGGCATG 3845
           -
Db   2450 - 2449

Qy   3846 GATGCGCGGATAGCCGCTGCTGGTTTCCTGGATGCCGACGGATTTGCACTGCCGGTAGAA 3905
           -
Db   2450 - 2449

Qy   3906 CTCCGCGGAGGTCGTCCAGCCTCAGGCAGCAGCTGAACCAACTCGCGAGGGGATCGAGCCC 3965
           -
Db   2450 - 2449

Qy   3966 GGGGGTGGGCGGCCGAAGAACTCCAGCATGAGATCCCGCGCTGAGGATCATCCAGCCGCGTC 4025
           -
Db   2450 - 2449

Qy   4026 CCGGAAAACGATTCCGAAGCCCAACCTTTCATAGAAGGCGGCGGTGGAATCGAAATCTCG 4085
           -
Db   2450 - 2449

Qy   4086 TGATGGCAGGTTGGGCGGTCGGTTCGTTGGTCGGTCATTTCGAACCCCAGAGTCCGCTCAGAAG 4145
           ||||||||| ||||||||
Db   2450 - - - - - - - - -   -CGCTCAGAAG 2459

Qy   4146 AACTCGTCAAGAAGGCGATAGAAGGCGATGCGCTGCGAATCGGGAGCGGCGATACCGTAA 4205
           |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2460 AACTCGTCAAGAAGGCGATAGAAGGCGATGCGCTGCGAATCGGGAGCGGCGATACCGTAA 2519

Qy   4206 AGCACGAGGAAGCGGTCAGCCCATTCGCCGCCAAGCTCTTCAGCAATATCACGGGTAGCC 4265
           |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2520 AGCACGAGGAAGCGGTCAGCCCATTCGCCGCCAAGCTCTTCAGCAATATCACGGGTAGCC 2579

Qy   4266 AACGCTATGTCCTGATAGCGGTCCGCCACACCCAGCCGGCCACAGTCGATGAATCCAGAA 4325
           |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2580 AACGCTATGTCCTGATAGCGGTCCGCCACACCCAGCCGGCCACAGTCGATGAATCCAGAA 2639

Qy   4326 AAGCGGCCATTTTCCACCATGATATTCGGCAAGCAGGCATCGCCATGGGTCACGACGAGA 4385
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Qy   4386 TCCTCGCCGTCGGGCATGCGCGCCTTGAGCCTGGCGAACAGTTCGGCTGGCGCGAGCCCC 4445
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Db   2700 TCCTCGCCGTCGGGCATGCGCGCCTTGAGCCTGGCGAACAGTTCGGCTGGCGCGAGCCCC 2759

Qy   4446 TGATGCTCTTCGTCCAGATCATCCTGATCGACAAGACCGGCTTCCATCCGAGTACGTGCT 4505
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Db   2760 TGATGCTCTTCGTCCAGATCATCCTGATCGACAAGACCGGCTTCCATCCGAGTACGTGCT 2819

Qy   4506 CGCTCGATGCGATGTTTCGCTTGGTGGTGTCGGTGAATGGGCAGGTAGCCGGATCAAGCGTATGC 4565
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Db   2820 CGCTCGATGCGATGTTTCGCTTGGTGGTGTCGGTGAATGGGCAGGTAGCCGGATCAAGCGTATGC 2879

Qy   4566 AGCCGCGCCATTGCATCGCATCGATGGATACTTCTCGCGAGGAGCAAGGTGAGATGAC 4625
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Qy   4686 ACGTCGAGCACAGCTGCGCAAGGAACGCCCGTCGTGGCCCAGCCACGATAGCCGCGCTGCC 4745
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Qy   4746 TCGTCCTGCAGTTCATTCAGGGCACCGGACAGGTCGTCTTGACAAAAAGAACCGGGGC 4805
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Qy   4806 CCCTGGCTGACACAGCCGGAACACGGGGCCATCAGAGCAGCCGATTGCTGTCGTTGTGCCCAG 4865
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Qy   4926 TCAATCATGCGAAACGATCCTCATCCTGTCTCTTGATCAGATCTTGATCCCTGCGCCAT 4985
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Qy   5106 TATCGCCATGTAAGCCCACTGCAAGCTACCTGCTTTCTCTT 5146
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Db   3420 AACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGCTATT 3460

RESULT 15
AAL62059
ID   AAL62059 standard; DNA; 3534 BP.
XX
AC   AAL62059;
XX
DT   22-SEP-2003   (first entry)
XX
DE   TI-GHRH plasmid DNA.
XX
KW   Plasmid-mediated supplementation; anaemia; tumour; adenoma; melanoma;
KW   sarcoma; immune dysfunction; carcinoma; leukaemia; kidney failure;
KW   lymphoma; weight loss; lymphopoesis; appetite stimulant; anoretic;
KW   growth hormone releasing hormone; GHRH; cyclic; circular; gene; ds.
XX
OS   Unidentified.
XX
PN   WO2003049700-A2.
XX
PD   19-JUN-2003.
XX
PF   10-DEC-2002; 2002WO-US039509.
XX
PR   11-DEC-2001; 2001US-0339610P.
XX
PA   (ADVI-) ADVISYS INC.

PA (BAYU) BAYLOR COLLEGE MEDICINE.
XX
PI Draghia-Akli R, Carpenter RH, Kern DR, Schwartz RJ, King G;
PI Hahn K, Brenner MK;
XX
DR WPI; 2003-558968/52.
XX
PT Treating anemia, immune dysfunction, tumor, increasing total red blood
PT cell mass, reversing wasting or abnormal weight loss in subject, by
PT administering nucleic acid construct encoding growth-hormone-releasing-
PT hormone.
XX
PS Claim 4; Page 191-193; 212pp; English.
XX
CC The invention relates to compositions and methods for plasmid-mediated
CC supplementation. The method is useful for treating anaemia, tumour (such
CC as adenoma, mast cell tumour, melanoma, sarcoma or solid tumour), immune
CC dysfunction, carcinoma (benign or malignant), leukaemia, lymphoma or
CC kidney failure, for preventing the development of metastatic tumour, for
CC increasing total red blood cell mass, for reversing wasting, abnormal
CC weight loss or suppression of lymphopoesis, in a subject, or for
CC increasing weight gain in a chronically ill subject or, or for extending
CC life expectancy for a chronically ill subject. The present sequence is TI
CC -growth hormone releasing hormone (GHRH) plasmid DNA. This sequence is
CC used to illustrate the method of the invention
XX
SQ Sequence 3534 BP; 764 A; 1017 C; 978 G; 775 T; 0 U; 0 Other;

Query Match   30.4%;   Score 1603.8; DB 9; Length 3534;
Best Local Similarity   82.8%;   Pred. No. 2.5e-234;
Matches 2022; Conservative   0; Mismatches   27; Indels 392; Gaps   1;

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Qy   2946 CGCTTCCTCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGC 3005
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Qy   3066 GTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTT 3125
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Qy   3126 CCATAGGCTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCG 3185
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Qy   3186 AAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTC 3245
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Qy    4986 CAGATCCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTGCAGGGCTTCCAACCTTACCA 5045
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Db    3360 GAGGGCGCCCCAGCTGCAATTCCGGTTCGCTTGCTGTCCATAAAACCGCCCAGTCTAGC 3419

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Db    3420 AACTGTTGGGAAGGGGCATCGGTGCGCGGCCTTCTTCGCTATT 3460
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                    GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on:        July  2, 2005, 20:36:53 ; Search time 792 Seconds
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Searched:       1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters:     2405568

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

                        SUMMARIES
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c 1	2240	42.4	8349	4	US-09-186-002-16	Sequence 16, Appl
c 2	1793.4	33.9	4800	4	US-09-554-929-1	Sequence 1, Appl
c 3	1652.4	31.3	5594	3	US-09-380-190A-29	Sequence 29, Appl
c 4	1618.2	30.6	6561	3	US-09-380-190A-30	Sequence 30, Appl
c 5	1602.2	30.3	5707	2	US-08-472-809B-8	Sequence 8, Appl
c 6	1571.6	29.7	4665	3	US-08-948-378A-7	Sequence 7, Appl
c 7	1571.6	29.7	4665	4	US-09-169-425C-7	Sequence 7, Appl
c 8	1571.6	29.7	4665	4	US-09-759-960-7	Sequence 7, Appl
c 9	1570	29.7	4518	3	US-09-380-190A-26	Sequence 26, Appl
c 10	1570	29.7	4886	4	US-09-533-220A-4	Sequence 4, Appl
c 11	1570	29.7	6139	2	US-08-751-767A-7	Sequence 7, Appl
c 12	1569.8	29.7	4748	4	US-09-796-575-4	Sequence 4, Appl
c 13	1569.8	29.7	4992	4	US-09-796-575-5	Sequence 5, Appl
c 14	1569.8	29.7	5069	4	US-09-393-483A-1	Sequence 1, Appl
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c 19	1569.8	29.7	11093	5	PCT-US96-10041-5	Sequence 40, Appl
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c 21	1501.4	28.4	6795	3	US-09-380-190A-22	Sequence 3, Appl
c 22	1501.4	28.4	8574	3	US-09-554-572-3	Sequence 23, Appl
c 23	1501.4	28.4	9093	3	US-09-380-190A-23	Sequence 2, Appl
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c 25	1501.4	28.4	9145	4	US-09-554-572-1	Sequence 20, Appl
c 26	1501	28.4	4958	3	US-09-380-190A-20	Sequence 18, Appl
c 27	1501	28.4	5754	3	US-09-380-190A-18	Sequence 19, Appl

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c 31	1501	28.4	6359	3	US-09-380-190A-15	Sequence 15, Appl
c 32	1501	28.4	6891	3	US-09-380-190A-16	Sequence 16, Appl
c 33	1501	28.4	8657	3	US-09-380-190A-14	Sequence 14, Appl
c 34	1490.4	28.2	3974	3	US-09-026-343-33	Sequence 33, Appl
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c 37	1490.4	28.2	3974	3	US-09-023-082A-147	Sequence 147, App
c 38	1490.4	28.2	3974	3	US-09-044-855A-7	Sequence 7, Appl
c 39	1490.4	28.2	3974	3	US-09-078-670-4	Sequence 4, Appl
c 40	1490.4	28.2	3974	3	US-09-026-408-14	Sequence 14, Appl
c 41	1490.4	28.2	3974	3	US-09-362-871-33	Sequence 33, Appl
c 42	1490.4	28.2	3974	3	US-09-627-154-4	Sequence 4, Appl
c 43	1490.4	28.2	3974	4	US-09-027-287-50	Sequence 50, Appl
c 44	1490.4	28.2	3974	4	US-09-437-602-4	Sequence 4, Appl
c 45	1490.4	28.2	3974	4	US-09-252-656B-50	Sequence 50, Appl

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                        ALIGNMENTS

RESULT 1
US-09-186-002-16
;  Sequence 16, Application US/09186002B
;  Patent No. 6489542
;  GENERAL INFORMATION:
;  APPLICANT: Corbin, David R.
;  APPLICANT: Romano, Charles P.
;  TITLE OF INVENTION: Improved Method for Transforming Plants to Express
;  TITLE OF INVENTION: delta-Endotoxins
;  FILE REFERENCE: 38-21(13547) US Pat No. 6489542 09/186,002
;  CURRENT APPLICATION NUMBER: US/09/186,002B
;  CURRENT FILING DATE: 1998-11-04
;  NUMBER OF SEQ ID NOS: 18
;  SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 16
;  LENGTH: 8349
;  TYPE: DNA
;  ORGANISM: Artificial Sequence
;  FEATURE:
;  NAME/KEY: gene
;  LOCATION: (3666)..(5573)
;  OTHER INFORMATION: completely synthesized
US-09-186-002-16

Query Match             42.4%;      Score 2240;  DB 4;  Length 8349;
Best Local Similarity   93.4%;      Pred. No. 0;
Matches 2409;  Conservative    0;  Mismatches    25;  Indels 144;  Gaps  1;

Qy    2706 CTAGACGTAATCATGGTCATAGCTGTTCCTGTGTGAAATTGTTATCCGCTCACAATTCC 2765
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5911 CTTGGCGTAATCATGGTCATAGCTGTTCCTGTGTGAAATTGTTATCCGCTCACAATTCC 5970

Qy    2766 ACACAACATACGAGCCCGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTA 2825
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5971 ACACAACATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTA 6030

Qy    2826 ACTCACATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCA 2885
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    6031 ACTCACATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCA 6090

Qy    2886 GCTGCATTAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTC 2945
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    6091 GCTGCATTAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTC 6150

Qy    2946 CGCTTCCTCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGGCGGAGCGGTATCAGC 3005
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    6151 CGCTTCCTCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGGCGGAGCGGTATCAGC 6210

Qy    3006 TCACTCAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAAACGCAGGAAAGAACAT 3065
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db  6211  TCACTCAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACAT  6270

Qy  3066  GTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTT  3125
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  6271  GTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTT  6330

Qy  3126  CCATAGGCTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCG  3185
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  6331  CCATAGGCTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCG  6390

Qy  3186  AAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTC  3245
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  6391  AAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTC  6450

Qy  3246  TCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGT  3305
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  6451  TCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGT  6510

Qy  3306  GGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAA  3365
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  6511  GGCGCTTTCTCAATGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAA  6570

Qy  3366  GCTGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCGGTAACTA  3425
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  6571  GCTGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTA  6630

Qy  3426  TCGTCTTGAGTCCAACCCGGTAAGACAGCACTTATCGCCACTGGCAGCAGCCACTGGTAA  3485
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  6631  TCGTCTTGAGTCCAACCCGGTAAGACAGCACTTATCGCCACTGGCAGCAGCCACTGGTAA  6690

Qy  3486  CAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAA  3545
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  6691  CAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAA  6750

Qy  3546  CTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTT  3605
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  6751  CTACGGCTACACTAGAAGGACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTT  6810

Qy  3606  CGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTT  3665
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  6811  CGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTT  6870

Qy  3666  TTTTGTTTGCAAGCAGCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGAT  3725
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  6871  TTTTGTTTGCAAGCAGCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGAT  6930

Qy  3726  CTTTTCTACGGGGTCTGACGCTCAGTGGAACGAAAACTCACGTTAAGGGATTTTGGTCAT  3785
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  6931  CTTTTCTACGGGGTCTGACGCTCAGTGGAACGAAAACTCACGTTAAGGGATTTTGGTCAT  6990

Qy  3786  GAGATTATCGTGACCAAAGCGGCCATGTGCCTCCCCACTCGTGCGGTTCGGGGGCATG  3845
          |||||||||||||||||||||||||||||||||||||||||||| |
Db  6991  GAGATTATCAAAAAGGATCTTCACCTAGATCCTT------------------------  7024

Qy  3846  GATGCGGCGATAGCCGCTGCTGGTTCCTGGTTCCTGCTGCGCGGATTTGCACTGCCGGTAGAA  3905
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db            ------------------------------------------------------  7025

Qy  3906  CTCCGCGAGGTGTCGTCCAGCCTCGAGCAGCTGAACCAACTCGCCGAGGGGATCGAGCCC  3965
          |                                                          ||
Db            --------------------------------------------------------TT  7026

Qy  3966  GGGGTGGCGGAAGAACTCCGCCGCATGAGAGGATCATCCCAGCCTGAGGATCATCCAGCC  4025
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  7027  GGGGTGGCGGAAGAACTCCGCCGCATGAGAGGATCATCCCAGCCTGAGGATCATCCAGCC  7086

Qy  4026  CCGGAAAAAGAGATTCCGGAAGCCCAACCCTTCATAGAAGGCGGCGGTGGAATCTCG  4085
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  7087  CCGGAAAAAGAGATTCCGGAAGCCCAACCCTTCATAGAAGGCGGCGGTGGAATCTCG  7146

Qy  4086  TGATGGCAGGTTGGGCGTCGCTTGGTCGTCGGTCATTTCGAACCCCATTTCGAACCCCGCTCCGGTCCCGCTCCAGAAG  4145
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  7147  TGATGGCAGGTTGGGCGTCGCTTGGTCGTCGGTCATTTCGAACCCCATTTCGAACCCCGCTCCGGTCCCGCTCCAGAAG  7206
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Qy  4146  AACTCGTCAAGAAGGCGGATAGAAGGCCGATGCGGCTGCGAATCGGCAGCGGCGGATACCGTAA  4205
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  7207  AACTCGTCAAGAAGGCGGATAGAAGGCCGATGCGGCTGCGAATCGGCAGCGGCGGATACCGTAA  7266

Qy  4206  AGCACGAGGAGCGGTCAGCCGTTCGCCGCCAAGCTCTTCAGCAATATCACGGGTAGCC  4265
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  7267  AGCACGAGGAGCGGTCAGCCGTTCGCCGCCAAGCTCTTCAGCAATATCACGGGTAGCC  7326

Qy  4266  AACGCTATGTCCTGATAGCGGTCCGCCACCAGCCGACCAGTGCGATGAATCCAGAA  4325
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  7327  AACGCTATGTCCTGATAGCGGTCCGCCACCAGCCGACCAGTGCGATGAATCCAGAA  7386

Qy  4326  AAGCGGCCATTTTCCACCATGATATTCGGCAAGCAGGCATCCCATGGGTCACGACGAGA  4385
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  7387  AAGCGGCCATTTTCCACCATGATATTCGGCAAGCAGGCATCGCATGGGTCACGACGAGA  7446

Qy  4386  TCCTCGCCGTGGGCATGCGCGCCTTGAGCCTGGCGAACAGTTCGGCTGGCGCGAGCCCC  4445
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  7447  TCCTCGCCGTCGGGCATGCGCGCCTTGAGCCTGGCGAACAGTTCGGCTGGCGCGAGCCCC  7506

Qy  4446  TGATGCTCTTCGTCCAGATCATCGATGCAGCAAGACGCCGGCTTCATCCGAGTACGTGCT  4505
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  7507  TGATGCTCTTCGTCCAGATCATCGATGCAGCAAGACGCCGGCTTCATCCGAGTACGTGCT  7566

Qy  4506  CGCTCGATGCGATGTTTCGCTTGGTGGTGTCGAATGGGCAGGAGCAGGTAGCCGGATCAAGCGTATGC  4565
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  7567  CGCTCGATGCGATGTTTCGCTTGGTGGTGTCGAATGGGCAGGAGCAGGTAGCCGGATCAAGCGTATGC  7626

Qy  4566  AGCCGCCGCATTGCATCAGCCATGATGGATACTTTCTCGGCAGGAGCAAGGTGAGATGAC  4625
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  7627  AGCCGCCGCATTGCATCAGCCATGATGGATACTTTCTCGGCAGGAGCAAGGTGAGATGAC  7686

Qy  4626  AGGAGATCTCCTGCCCCGCACTTCGCCCAAGGAACCTGCCCAGTAGCGCCGCTGCC  4685
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  7687  AGGAGATCCTGCCCCGCACTTCGCCCAAGGAACCTGCCCAGTAGCGCCGCTGCC  7746

Qy  4686  ACGTCGAGCACAGCTGCGCCAAGAACCCCGTCGTGGCCAGCCACGATAGCCGCGCTGCC  4745
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  7747  ACGTCGAGCACAGCTGCGCCAAGAACCCCGTCGTGGCCAGCCACGATAGCCGCGCTGCC  7806

Qy  4746  TCGTCCTGCAGTTCATTCAGGGCACCGGACAGGTCGGTCTTGACAAAAAGAACCGGGCGC  4805
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  7807  TCGTCCTGCAGTTCATTCAGGGCACCGGACAGGTCGGTCTTGACAAAAAGAACCGGGCGC  7866

Qy  4806  CCCTGCGCTGACAGCCGGAACACGGGCGGCATCAGAGCAGCCGATTGTCTGTTGTGCCCAG  4865
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  7867  CCCTGCGCTGACAGCCGGAACACGGGCGGCATCAGAGCAGCCGATTGTCTGTTGTGCCCAG  7926

Qy  4866  TCATAGCCGAATAGCCTCTCCACCCAAGCGGCCGGAGAACCTGCGTGCAATCCATCTTGT  4925
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  7927  TCATAGCCGAATAGCCTCTCCACCCAAGCGGCCGGAGAACCTGCGTGCAATCCATCTTGT  7986

Qy  4926  TCAATCATGCGAAACGATCCTCGTCTCTTGATCAGATCTTGATCCCCTGCGCCAT  4985
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  7987  TCAATCATGCGAAACGATCCTCGTCTCTTGATCAGATCTTGATCCCCTGCGCCAT  8046

Qy  4986  CAGATCCTTGGCCGCGAAGCCGCCATCCAGTTTACTTTGCAGGGCTTCCCAACCTTACCA  5045
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  8047  CAGATCCTTGGCCGCCGAAGCAGCCATCCAGTTTACTTTGCAGGGCTTCCCAACCTTACCA  8106

Qy  5046  GAGGGCGCCCCAGCTGGCAATTCCGGTTCGCTTGCTGTCCATAAAACCGCCCAGTCTAGC  5105
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  8107  GAGGGCGCCCCAGCTGGCAATTCCGGTTCGCTTGCTGTCCATAAAACCGCCCAGTCTAGC  8166

Qy  5106  TATCGGCCATGTGAAGTGCAAAGTCCACTCGCTTTCTCTTTGCGCTTGCGTTTTCCCTT  5165
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  8167  TATCGGCCATGTGAAGTGCAAAGTCCACTCGCTTTCTCTTTGCGCTTGCGTTTTCCCTT  8226

Qy  5166  GTCCAGATAGCCCAGTAGCTGACATTCATCCGGGGTCAGCACCGTTTCTGCGGACTGGCT  5225
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  8227  GTCCAGATAGCCCAGTAGCTGACATTCATCCGGGGTCAGCACCGTTTCTGCGGACTGGCT  8286
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Qy 5226 TTCTACGTGTTCCGCTTCCTTTAGCAGCCCTTGCGCCCTGAGTGCTTGCGGCAGCGTG 5283
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 8287 TTCTACGTGTTCCGCTTCCTTTAGCAGCCCTTGCGCCCTGAGTGCTTGCGGCAGCGTG 8344

RESULT 2
US-09-554-929-1/c
; Sequence 1, Application US/09554929
; Patent No. 6521427
; GENERAL INFORMATION:
; APPLICANT: Evans, Glen A.
; TITLE OF INVENTION: A Method for the Complete Chemical
; TITLE OF INVENTION: Synthesis and Assembly of Genes and Genomes
; FILE REFERENCE: P-EA 4749
; CURRENT APPLICATION NUMBER: US/09/554,929
; CURRENT FILING DATE: 2000-05-12
; NUMBER OF SEQ ID NOS: 193
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 4800
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic plasmid
US-09-554-929-1

Query Match   33.9%; Score 1793.4; DB 4; Length 4800;
Best Local Similarity 91.8%; Pred. No. 0;
Matches 1980; Conservative 0; Mismatches 1; Indels 176; Gaps 1;

Qy 3787 AGATTATCGTGACCAAAGCGGCCATCGTGCCTGCCTCCCCACTCCTGCGCAGTTCGGGGGGCATGG 3846

Db 4141 --- 4142

Qy 3847 ATGCGGGGATAGCCGCTGCTGGTTTCCTGGATGCCGACGGATTGCACTGCCGGTAGAAC 3906

Db 4141 -- 4142

Qy 3907 TCCGCGGAGTCGTCCAGCCTCAGGCAGCAGCTGCAACCACTCGCGAGGGGATCGAGCGCCG 3966
                                                              |||||
Db 4141 --GCCCG 4137

Qy 3967 GGGTGGGCGGAAGAACTCAGCATGAGATCCCCGCTGGAGGATCATCCAGCCGCCGCGTCC 4026
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4136 GGGTGGGCGGAAGAACTCAGCATGAGATCCCCGCTGGAGGATCATCCAGCCGCCGCGTCC 4077

Qy 4027 CGGAAAACGATTCCGAAGCCCAACCTTTCATAGAGAGGCGTGGAATCGAAATCTCGT 4086
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4076 CGGAAAACGATTCCGAAGCCCAACCTTTCATAGAGAGGCGTGGAATCGAAATCTCGT 4017

Qy 4087 GATGGCAGGTTGGGCGTCGCTTGGTCGTCATTTGGCGTCGCTTGGTCGTCATTTCGAAT 4146
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4016 GATGGCAGGTTGGGCGTCGCTTGGTCGTCATTTCGAACCCCAGAGTCCCGCTCAGAAGA 3957

Qy 4147 ACTCGTTCAAGAAGGCGATAGAAGGCGATAGCGTTGCGAATCGGGAGGCGGGCGATACCGTAAA 4206
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3956 ACTCGTTCAAGAAGGCGATAGAAGGCGATAGCGTTGCGAATCGGGAGGCGGGCGATACCGTAAA 3897

Qy 4207 GCACGAGGAAGCCGGTCAGCAGCATCACAAAAATGACGCTCAAGTCAGAGGTGGCGA 4266
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3896 GCACGAGGAAGCCGGTCAGCAGCATCACAAAAATGACGCTCAAGTCAGAGGTGGCGA 3837

Qy 4267 ACGCTATGTCTGATAGCGGTCCGGCGTTCCCCTGGAAGCTCCCTCGTGCGCTCT 4326
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3836 ACGCTATGTCTGATAGCGGTCCGGCGTTCCCCTGGAAGCTCCCTCGTGCGCTCT 3777

Qy 4327 AGGGGCCATTTCCACCATGATATTCGGCAAGCAGGCATCGCCATGGGTCACGACGAGAT 4386
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3776 AGCGGCCATTTCCACCATGATATTCGGCAAGCAGGCATCGCCATGGGTCACGACGAGAT 3717

Qy 4387 CCTCGCCGTCGGGCATGCCGCGCTTGAGCGTTCGGTGTAGTCGTTCGCTCCAAG 4446
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3716 CCTCGCCGTCGGGCATGCCGCGCTTGAGCGTTCGGTGTAGTCGTTCGCTCCAAG 3657

Qy 4447 GATGCTCTTCGTCCAGATCATCCTGGTTCATGGCGACCGCTTCAGCCGCCAGTGTACTAAACTAT 4506
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3656 GATGCTCTTCGTCCAGATCATCCTGATGTCCAGATCATCCTGATGTCCGCTTCATCCGAGTACGTGCTC 3597

Qy 4507 GCTCGATGCGATGTTTCGCTTGGTGGTCGAATGGCAGTGGGCAGGTAGCCGGATCAAGCGTATGCA 4566
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3596 GCTCGATGCGATGTTTCGCTTGGTGGTCGAATGGGTCGAATGGCAGTGGGCAGGTAGCCGGATCAAGCGTATGCA 3537

Qy 4567 GCCGCCGCCATTGCATCAGCCATGATGGATACTTTCTCGGCAGCAGGTGGTGGGCCTAAC 4626
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3536 GCCGCCGCCATTGCATCAGCCATGATGGATGCAGCGCCATTGCATCAGCCATGATGGATACTTTCTCGGCAGCAGGTGGTGGGCCTAAC 3477

Qy 4627 GGAGATCCTGCCCCGGCACTTCGCCCAATAGCAGCCAGTCCCTTCCCGGCTGGATCCTTACCTTC 4686
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3476 GGAGATCCTGCCCCGGCACTTCGCCCAATAGCAGCCAGTCCCTTCCCGGCTGGATCCTTACCTTC 3417

Qy 4687 CGTCGAGCACAGCTGCGCAAGGAACGCCCGTCGTGGCCAGCCACGATAGCCGCGCTGCCT 4746
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3416 CGTCGAGCACAGCTGCGCAAGGAACGCCCGTCGTGGCCAGCCACGATAGCCGCGCTGCCT 3357

Qy 4747 CGTCCTGCAGTTCATTCAGGGCACCGGACAGGTCGGTCTTGACAAAAAGAACCGGGCGCC 4806
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3356 CGTCCTGCAGTTCATTCAGGGCACCGGACAGGTCGGTCTTGACAAAAAGAACCGGGCGCC 3297

Qy 4807 CCTGCGCTGACAGCCGGAACACGGCGGCATCAGAGCAGCCGATTGTCTGTTGTGCCCAGT 4866
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3296 CCTGCGCTGACAGCCGGAACACGGCGGCATCAGAGCAGCCGATTGTCTGTTGTGCCCAGT 3237

Qy 3127 CATAGGCTCCGCCCCCCTGACGAGCATCACAAAAATGACGCTCAAGTCAGAGGTGGCGA 3186
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4800 CATAGGCTCCGCCCCCCTGACGAGCATCACAAAAATGACGCTCAAGTCAGAGGTGGCGA 4741

Qy 3187 AACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCTGGAAGCTCCCTCGTGCGCTCT 3246
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4740 AACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCTGGAAGCTCCCTCGTGCGCTCT 4681

Qy 3247 CCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTG 3306
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4680 CCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTG 4621

Qy 3307 GCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAG 3366
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4620 GCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAG 4561

Qy 3367 CTGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTAT 3426
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4560 CTGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTAT 4501

Qy 3427 CGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAAC 3486
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4500 CGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAAC 4441

Qy 3487 AGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAAC 3546
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4440 AGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAAC 4381

Qy 3547 TACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTC 3606
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4380 TACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTC 4321

Qy 3607 GGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTT 3666
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4320 GGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTT 4261

Qy 3667 TTTGTTTGCAAGCAGCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGATC 3726
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4260 TTTGTTTGCAAGCAGCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGATC 4201

Qy 3727 TTTTCTACGGGTCTGACGCTCAGTGGAACGAAAACTCACGTTAAGGGATTTTGGTCATG 3786
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4200 TTTTCTACGGGTCTGACGCTCAGTGGAACGAAAACTCACGTTAAGGGATTTTGGTCAT- 4142

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Query Match
Best Local Similarity   31.3%;   Score 1652.4;   DB 3;   Length 5594;
                        85.4%;   Pred. No. 0;
Matches 1916;   Conservative 0;   Mismatches 261;   Indels 67;   Gaps 4;

Qy 3107 CCGCGGTTGCTGGCGTTTTCATAGCTCCGCCCCCTGACGAGCATCACAAAAATCGAC 3166
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 5591 CGGCGGTTGCTGGCGTTTTCATAGCTCCGCCCCCTGACGAGCATCACAAAAATCGAC 5532

Qy 3167 GCTCAAGTCAGAGGTGCGCAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCTG 3226
        ||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db 5531 GCTCAAGTCAGAGGTGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCTG 5472

Qy 3227 GAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCT 3286
        ||||||||||||||||||||||||||||||||||||||| |||||||||||||||||||
Db 5471 GAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGCCTTACCGGATACCTGTCCGCCT 5412

Qy 3287 TTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGG 3346
        ||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Db 5411 TTCTCCCTTCGGGAAGCGTGGCGCTTTCTCAATGCTCACGCTGTAGGTATCTCAGTTCGG 5352

Qy 3347 TGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCT 3406
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 5351 TGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCT 5292

Qy 3407 GCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACGACTTATCGCCAC 3466
        ||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db 5291 GCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCAC 5232

Qy 3467 TGGCAGCAGCCACTGGTAACAGGATTAGCAGCAGGAGGTATGTAGGCGGTGCTACAGAGT 3526
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 5231 TGGCAGCAGCCACTGGTAACAGGATTAGCAGCAGGAGGTATGTAGGCGGTGCTACAGAGT 5172

Qy 3527 TCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTC 3586
        |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db 5171 TCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGGACAGTATTTGGTATCTGCGCTC 5112

Qy 3587 TGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAACCA 3646
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Db 5111 TGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAACCA 5052

Qy 3647 CCGCTGGTAGCGGTGGTTTTTTTGTTTGCAAGCAGCAGATTACGCGCAGAAAAAAAGGAT 3706
        |||||||||||||||||||||||||||||||||||||||||||  |||||  |
Db 5051 CCGCTGGTAGCGGTGGTTTTTTTGTTTGCAAGCAGCAGATTACTGCGCCCGAGTGAGG 4992

Qy 3707 CTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCTC---------AGTGGAACG 3757
        ||||  |||||| ||    |  |||| |||||||     | |          |||||||
Db 4991 GGGTTGTGGGGCTCTTTTATTGACCTCGGGGAGCGGGAGCGGGAACAGAGGCGAGAAGCG 4932

Qy 3758 AAAACTCACGTTAAGGGATTTTGGTCATGAGATTATCGTCGACCAAAGCGGCCATCGTGC 3817
        ||  ||||  | ||  |    ||| |||||    |  ||   ||||||||||||||||||
Db 4931 AACTGATTGGTTAGTTGAAATAAGGCACAGGGTCATTTCAGGTCCTTGGGGCACCCTGGA 4872

Qy 3818 CTC-----------CCCACTTCTGCAGTTCGGGGATGCCATGGATGATGAGCCGGCTG 3864
        |||            |  ||| || ||||   |     | ||||| |||||
Db 4871 AACATCTGATGGTTCTCTAGAAACTGCTGAGGGCTGGACACCGGCTGGGGACCATCTGTT 4812

Qy 3865 CTGGTTTCCTGATGCCGACGGATTTGC-------ACTGCCGGTAGAACTCCGGCGAG 3914
        |||   |     |  | |  ||||| |           | |||||||||||||  |
Db 4811 CTTGGCCCTGAGCCGGGGCAGGAACTGCTTACCACAGATATCCGATTTGTTGGCCCATATTCA 4752

Qy 3915 GTCGTCCAGCCTCAGCGAGCAGCTGAACCAACTCGGCAGAGGGGATCGGGGTCGGGC 3974
        |||||  ||| | | |   | || |||||  || ||| |||  | || ||||  || |
Db 4751 GTCGTTCCATCTGTTCTTGGGGCCCGGGGCAGGAACTGCTTACCACAGATATCCTG 4692

Qy 3975 GAAGAACTCCAGCATGAGATCCCCGCCGCTGGAGGATCATCCAGCCGGCGTCCCGGAAAAC 4034
        ||||||  |  ||| |  | |  | |  ||  |   ||  | || ||  |   | |||
Db 4691 TTTGGCCCCATATTCAGCTGTTCCATCTGTTCGACCTTGATCGAATCGAAATCGG 4632

Qy 4035 GATTCCGAAGCCCAACCTTCATCAGAAGGCGGCGGTGAATCAAATCTCG-------- 4085
        ||| ||||| |||| |  |||||| |||| |  ||||  |  |||| |||
Db 4631 AGTTATGTATTTTTCCATGCCTTGCAAAATGGCGTTACTTAAGCTAGCTTGCCAAACCTA 4572

Qy 4867 CATAGCCGAATAGCCTCTCCACCCAAGCGGCCGGAGAACCTGCGTGCAATCCATCTGTT 4926
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3236 CATAGCCGAATAGCCTCTCCACCCAAGCGGCCGGAGAACCTGCGTGCAATCCATCTGTT 3177

Qy 4927 CAATCATGCGAAACGATCCTCATCCTGTCTCATCCGTCTTGATCAGATCTTGATCCCCTGCGGCCATC 4986
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3176 CAATCATGCGAAACGATCCTCATCCTGTCTCATCCGTCTTGATCAGATCTTGATCCCCTGCGGCCATC 3117

Qy 4987 AGATCCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTGCAGGGCTTCCCAACCTTACCAG 5046
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3116 AGATCCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTGCAGGGCTTCCCAACCTTACCAG 3057

Qy 5047 AGGGCGCCCCAGCTGGCAATTCCGGTTCGCTTGCTGTCCATAAAACCGCCCAGTCTAGCT 5106
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3056 AGGGCGCCCCAGCTGGCAATTCCGGTTCGCTTGCTGTCCATAAAACCGCCCAGTCTAGCT 2997

Qy 5107 ATCGCCATGTAAGCCCACTGCAAGCTACCTGCTTTCTCTTTGCGCTTGCGTTTTCCCTTG 5166
        ||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db 2996 ATCGCCATGTAAGCCCACTGCAAGCTACCTGCTTTCTCTTTGCGCTTGCGTTTTCCCTTG 2937

Qy 5167 TCCAGATAGCCCAGTAGCTGACATTCATCCGGGGTCAGCACCGTTTCTGCGGACTGGCTT 5226
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2936 TCCAGATAGCCCAGTAGCTGACATTCATCCGGGGTCAGCACCGTTTCTGCGGACTGGCTT 2877

Qy 5227 TCTACGTGTTCCGCTTCCTTTAGCAGCCCTTGCGCCCTGAGTGCTTGCGGCAGCGTG 5283
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2876 TCTACGTGTTCCGCTTCCTTTAGCAGCCCTTGCGCCCTGAGTGCTTGCGGCAGCGTG 2820
```

RESULT 3
US-09-380-190A-29/c
; Sequence 29, Application US/09380190A
; Patent No. 6410220
; GENERAL INFORMATION:
;   APPLICANT: NATURE TECHNOLOGY CORPORATION, ET AL.
;   TITLE OF INVENTION: SELF-ASSEMBLING GENES, VECTORS AND USES
;   THEREOF
;   NUMBER OF SEQUENCES: 74
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: MUETING, RAASCH & GEBHARDT, P.A.
;   STREET: 119 NORTH FOURTH STREET, SUITE 203
;   CITY: MINNEAPOLIS
;   STATE: MINNESOTA
;   COUNTRY: USA
;   ZIP: 55401
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/380,190A
;   FILING DATE: 26-Aug-1999
;   CLASSIFICATION: <Unknown>
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: PCT/US98/03918
;   FILING DATE: 28-FEB-98
;   ATTORNEY/AGENT INFORMATION:
;   NAME: MUETING, ANN M.
;   REGISTRATION NUMBER: 33,977
;   REFERENCE/DOCKET NUMBER: 228.00010201
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 612-305-1217
;   TELEFAX: 612-305-1228
; INFORMATION FOR SEQ ID NO: 29:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 5594 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: DNA (genomic)
;   SEQUENCE DESCRIPTION: SEQ ID NO: 29:
US-09-380-190A-29

Qy   4086 --------------------TGATGGCAGGTTGGGCGTCGCTTGGTCGGTCATT 4119
                              ||||||||||||||||||||||||||||||||
Db   4571 CAGTTGGGGTCTTCATTCCCCCGTTTTCTGGAGGTTGGGCGTCGCTTGGTCGGTCATT 4512

Qy   4120 TCGAACCCCAGAGTCCCGCTCAGAAGAACTCGTCAAGAAGCCGATAGAAGGGCGATGCGCT 4179
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4511 TCGAACCCCAGAGTCCCGCTCAGAAGAACTCGTCAAGAAGCCGATAGAAGGGCGATGCGCT 4452

Qy   4180 GCGAATCGGGAGCGGCGATACCGTAAAGCACGAGGAAGCGGTCAGCCCATTCGCCGCCAA 4239
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4451 GCGAATCGGGAGCGGCGATACCGTAAAGCACGAGGAAGCGGTCAGCCCATTCGCCGCCAA 4392

Qy   4240 GCTCTTCAGCAATATCACGGGTAGCCAACGCTATGTCCTGATAGCGTCCGCCACACCCA 4299
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4391 GCTCTTCAGCAATATCACGGGTAGCCAACGCTATGTCCTGATAGCGTCCGCCACACCCA 4332

Qy   4300 GCCGCCACAGTCGATGAATCCAGAAAAGCGGCCATTTTCCACCATGATAATTCGGCAAGC 4359
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4331 GCCGGCCACAGTCGATGAATCCAGAAAAGCGGCCATTTTCCACCATGATAATTCGGCAAGC 4272

Qy   4360 AGCCATGCCATGGGTCACGACAGAGATCCTCCGCCGTCGGGCATGCGCCCTTGAGCCTCGG 4419
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4271 AGCCATGCCATGGGTCACGACAGAGATCCTCCGCCGTCGGGCATGCGCCCTTGAGCCTGG 4212

Qy   4420 CGAACAGTTCGGCTGGCGCGAGCCCCTGATGCTCTTCGTCCAGATCATCCTGATCGACAA 4479
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4211 CGAACAGTTCGGCTGGCGCGAGCCCCTGATGCTCTTCGTCCAGATCATCCTGATCGACACA 4152

Qy   4480 GACCGGCTTCCATCCGAGTACGTGCTCGCTCGATGCGATGTTTCGCTTGGTGTCGAATG 4539
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4151 GACCGGCTTCCATCCGAGTACGTGCTCGCTCGATGCGATGTTTCGCTTGGTGTCGAATG 4092

Qy   4540 GGCAGGTAGCCGGATCAAGCGTATGCAGCCGCGCCATTGCATCAGCCATGATGGATACTT 4599
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4091 GGCAGGTAGCCGGATCAAGCGTATGCAGCCGCGCCATTGCATCAGCCATGATGGATACTT 4032

Qy   4600 TCTCGCAGGAGCAAGGTGAGATGACAGGAGATCTCGCCCCGGCACTTCGCCCAATAGCA 4659
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4031 TCTCGCAGGAGCAAGGTGAGATGACAGGAGATCTCGCCCCGGCACTTCGCCCAATAGCA 3972

Qy   4660 GCCAGTCCCTTCCCGCTTCAGTGACAACGTCGAGCACAGCTGCGCAAGGAACGCCCGTCG 4719
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3971 GCCAGTCCCTTCCCGCTTCAGTGACAACGTCGAGCACAGCTGCGCAAGGAACGCCCGTCG 3912

Qy   4720 TGGCCAGCCACGATAGCCGGCGTCGTCCTTCATTCAGGGCACCGGACAGGT 4779
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3911 TGGCCAGCCACGATAGCCGGCGTCGTCCTTCATTCAGGGCACCGGACAGGT 3852

Qy   4780 CGGTCTTGACACAAAAGAAACCGGGGCGCCCTGCGCTGACAGCCGGAACACGGCGGCATCAG 4839
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3851 CGGTCTTGACACAAAAGAAACCGGGGCGCCCTGCGCTGACAGCCGGAACACGGCGGCATCAG 3792

Qy   4840 AGCAGGCCGATTGTCTGTTGTGCCCAGTCATAGCCGAATAGCCTCTCCACCCAAGCCGCCG 4899
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3791 AGCAGGCCGATTGTCTGTTGTGCCCAGTCATAGCCGAATAGCCTCTCCACCCAAGCCGCCG 3732

Qy   4900 GAGAACCTGCGTGCAATCCATCTTGTTCAATCATGCGAAACGATCCTCATCCTGTCTCTT 4959
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3731 GAGAACCTGCGTGCAATCCATCTTGTTCAATCATGCGAAACGATCCTCATCCTGTCTCTT 3672

Qy   4960 GATCAGATCTTGATCCCCGGCCATCAGATCCCGCCAAGAAGCCATCCAGTTTA 5019
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3671 GATCAGATCTTGATCCCCGGCCATCAGATCCCGCCAAGAAGCCATCCAGTTTA 3612

Qy   5020 CTTTGCAGGGCTTCCCAACCTTACCAGAGAGGCGCCCCAGCTGGCAATTCCGGTTCGCTTG 5079
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3611 CTTTGCGGGGCTTCCCAACCTTACCAGAGAGGCGCCCCAGCTGGCAATTCCGGTTCGCTTG 3552

Qy   5080 CTGTCCATAAAACCGCCCAGTCAGCTATCGCCAGTGTCAAGCTTCAAGCTACCTGCT 5139
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Db   3551 CTGTCCATAAAACCGCCCAGTCAGCTATCGCCAGTGTCAAGCTTCAAGCTACCTGCT 3492

Qy   5140 TTCTCTTTGCGCTTGCGTTTCCCTTGTCCCAGATAGCCCAGTAGCTGACATTCATCCGGG 5199
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db   3491 TTCTCTTTGCGCTTGCGTTTCCCTTGTCCCAGATAGCCCAGTAGCTGACATTCATCCGGG 3432

Qy   5200 GTCAGCACCGTTTCTGCGGACTGGCTTTCTCACGTGTTCCGCTTCCGCTTCCGCTTTAGCAGCCCTTGC 5259
           |||||||||||||||||||||||||||||||||||||||||||||||||
Db   3431 GTCAGCACCGTTTCTGCGGACTGGCTTTCTCACGTGTTCCGCTTCCGCTTTAGCAGCCCTTGC 3372

Qy   5260 GCCCTGAGTGCTTGCGGCAGCGTG 5283
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Db   3371 GCCCTGAGTGCTTGCGGCAGCGTG 3348

RESULT 4
US-09-380-190A-30/c
; Sequence 30, Application US/09380190A
; Patent No. 6410220
; GENERAL INFORMATION:
;   APPLICANT: NATURE TECHNOLOGY CORPORATION, ET AL.
;   TITLE OF INVENTION: SELF-ASSEMBLING GENES, VECTORS AND USES
;   THEREOF
;   NUMBER OF SEQUENCES: 74
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: MUETING, RAASCH & GEBHARDT, P.A.
;   STREET: 119 NORTH FOURTH STREET, SUITE 203
;   CITY: MINNEAPOLIS
;   STATE: MINNESOTA
;   COUNTRY: USA
;   ZIP: 55401
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/380,190A
;   FILING DATE: 26-Aug-1999
;   CLASSIFICATION: <Unknown>
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: PCT/US98/03918
;   FILING DATE: 28-FEB-98
;   ATTORNEY/AGENT INFORMATION:
;   NAME: MUETING, ANN M.
;   REGISTRATION NUMBER: 33,977
;   REFERENCE/DOCKET NUMBER: 228.00010201
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 612-305-1217
;   TELEFAX: 612-305-1228
; INFORMATION FOR SEQ ID NO: 30:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 6561 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: DNA (genomic)
;   SEQUENCE DESCRIPTION: SEQ ID NO: 30:
US-09-380-190A-30

Query Match   30.6%; Score 1618.2; DB 3; Length 6561;
Best Local Similarity   86.7%; Pred. No. 0;
Matches 1911; Conservative   0; Mismatches   23; Indels 269; Gaps   1;

Qy   3081 GCAAAGGCCAGGAACCGTAAAAAGCCGCGGTTGGCGTTTTCCATAGGCTCCGCCC 3140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2305 GCAGGTGTACTCGAGGCGGCGCATCTCGGCGGTTGCTGCGGCGTTTTCCATAGGCTCCGCCC 2246

Qy   3141 CCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACT 3200
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Db   2245 CCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACT 2186

Qy   3201 ATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCT 3260
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2185 ATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCT 2126

(DNA sequence alignment — query (Qy) and database (Db) rows with position numbers. Two alignment columns per physical row across the page.)

RESULT 5
US-08-472-809B-8
; Sequence 8, Application US/08472809B
; Patent No. 595564
; GENERAL INFORMATION:
; APPLICANT: Schwartz, Robert J.
; APPLICANT: DeMayo, Franco J.
; APPLICANT: O'Malley, Bert W.
; TITLE OF INVENTION: Expression Vector Systems and

```
;    TITLE OF INVENTION:  Method of Use
;    NUMBER OF SEQUENCES: 8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071-2066
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  Word Perfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/472,809B
;      FILING DATE:  June 7, 1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/209,846
;      FILING DATE:  March 9, 1994
;      APPLICATION NUMBER:  07/789,919
;      FILING DATE:  No. 592564ember 6, 1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard J.
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  214/212
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO: 8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  5707 bases
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;      MOLECULE TYPE:  cDNA
US-08-472-809B-8
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Query Match         30.3%;    Score 1602.2;    DB 2;    Length 5707;
Best Local Similarity  82.8%;    Pred. No. 0;
Matches 2021; Conservative  0; Mismatches 28; Indels 392; Gaps 1;

Qy  2706 CTAGAGTAATCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCC 2765
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Db  3514 CTTGGCGTAATCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCC 3573

Qy  2766 ACACAACATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTA 2825
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3574 ACACAACATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTA 3633

Qy  2826 ACTCACATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCA 2885
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3634 ACTCACATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCA 3693

Qy  2886 GCTGCATTAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTC 2945
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3694 GCTGCATTAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTC 3753

Qy  2946 CGCTTCCTCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGC 3005
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3754 CGCTTCCTCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGC 3813

Qy  3006 TCACTCAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACAT 3065
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3814 TCACTCAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACAT 3873

Qy  3066 GTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTT 3125
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3874 GTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTT 3933

Qy  3126 CCATAGGCTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCG 3185
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3934 CCATAGGCTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCG 3993

Qy  3186 AAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTC 3245
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3994 AAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTC 4053

Qy  3246 TCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGT 3305
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4054 TCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGT 4113

Qy  3306 GGCGCTTTCTCATAGCTCACGCTGTAGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAA 3365
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4114 GGCGCTTTCTCATAGCTCACGCTGTAGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAA 4173

Qy  3366 GCTGGGCTGTGTGCACGAACCCCCGTTCAGCCGACCGGCTGCGCCTTATCCGGTAACTA 3425
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4174 GCTGGGCTGTGTGCACGAACCCCCGTTCAGCCGACCGGCTGCGCCTTATCCGGTAACTA 4233

Qy  3426 TCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAA 3485
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4234 TCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAA 4293

Qy  3486 CAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAA 3545
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4294 CAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAA 4353

Qy  3546 CTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTT 3605
         ||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db  4354 CTACGGCTACACTAGAAGGACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTT 4413

Qy  3606 CGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTT 3665
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Db  4414 CGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTT 4473

Qy  3666 TTTTGTTTGCAAGCAGCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCTTTTGAT 3725
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Db  4474 TTTTGTTTGCAAGCAGCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCTTTTGAT 4533

Qy  3726 CTTTTCTACGGGGTCTGACGCTCAGTGGAACGAAAACTCACGTTAAGGGATTTTGGTCAT 3785
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Db  4534 CTTTTCTACGGGGTCTGA--------------- 4551

Qy  3786 GAGATTATCGTCGACCAAAGCGGCCATCGTGCCTCCCACTCCTGCCAGTTCGGGGGCATG 3845
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Qy  3846 GATGCGCCGGATAGCCGCTGCTGGTTTCCTGGATGCCGACGGATTTGCACTGCCGGTAGAA 3905
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Qy  3906 CTCCGGAGGTCGTCCAGCCTCAGGCAGCAGCTGAACCAACTCGGCGAGGGGGATCGAGCGCC 3965
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Qy  4086 TGATGGCAGGTTGGGGTGCGGTTCATTTCGAACCCCAGAGTCCGCTCCAGAAG 4145
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Qy  4146 AACTCGTCAAGAAGGCGATAGAAGGCGATGCGCTGCGAATCGGGAGCGGCGATACCGTAA 4205
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Db  4562 AACTCGTCAAGAAGGCGATAGAAGGCGATGCGCTGCGAATCGGGAGCGGCGATACCGTAA 4621
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APPLICANT: Hedley, Mary Lynn
TITLE OF INVENTION: IMMUNOGENIC PEPTIDES FROM
TITLE OF INVENTION: THE HPV E7 PROTEIN
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
  ADDRESSEE: Fish & Richardson, P.C.
  STREET: 225 Franklin Street
  CITY: Boston
  STATE: MA
  COUNTRY: US
  ZIP: 02110-2804
COMPUTER READABLE FORM:
  MEDIUM TYPE: Diskette
  COMPUTER: IBM Compatible
  OPERATING SYSTEM: Windows95
  SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/08/948,378A
  FILING DATE: 09-OCT-1997
PRIOR APPLICATION DATA:
  APPLICATION NUMBER:
  FILING DATE:
ATTORNEY/AGENT INFORMATION:
  NAME: Fraser, Janis K.
  REGISTRATION NUMBER: 34,819
  REFERENCE/DOCKET NUMBER: 08191/004001
TELECOMMUNICATION INFORMATION:
  TELEPHONE: 617-542-5070
  TELEFAX: 617-543-8906
  TELEX: 200154
INFORMATION FOR SEQ ID NO: 7:
  SEQUENCE CHARACTERISTICS:
    LENGTH: 4665 base pairs
    TYPE: nucleic acid
    STRANDEDNESS: single
    TOPOLOGY: circular
  MOLECULE TYPE: pBIOTOPEHPV
US-08-948-378A-7

Query Match 29.7%;   Score 1571.6;   DB 3;   Length 4665;
Best Local Similarity 86.3%;   Pred. No. 0;
Matches 1850;   Conservative 0;   Mismatches 114;   Indels 180;   Gaps 3;

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Qy 3008 ACTCAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACCAGGAAAGAACATGT 3067
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Db 2624 AATGCATGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACCAGGAAAGAACATGT 2565

Qy 3068 GAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGGGTTGCTGGCGTTTTTCC 3127
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Db 2564 GAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGGGTTGCTGGCGTTTTTCC 2505

Qy 3128 ATAGGCTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAA 3187
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Qy 3188 ACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTC 3247
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Qy 3248 CTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGG 3307
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Db 2324 CGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGC 2265

Qy 3368 TGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATC 3427
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Db 2264 TGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATC 2205

Qy 3428 GTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACA 3487
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Qy 4206 AGCACGAGGAAGCGGTCAGCCATTCGCGCAAGCTCTTCAGCAATATCACGGGTAGCC 4265
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Db 4622 AGCACGAGGAAGCGGTCAGCCATTCGCGCAAGCTCTTCAGCAATATCACGGGTAGCC 4681

Qy 4266 AACGGCTATGTCCTGATAGCGGTCCGCCACACCCAGCCGGCCACACCCAGTGAATCCAGAA 4325
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Db 4682 AACGGCTATGTCCTGATAGCGGTCCGCCACACCCAGCCGGCCACACCCAGTGAATCCAGAA 4741

Qy 4326 AAGCCGGCCATTTCCACCATGATATTCGGCAAGCAGCATCGCCATGGGTCACGACGAGA 4385
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Db 4742 AAGCCGGCCATTTCCACCATGATATTCGGCAAGCAGCATCGCCATGGGTCACGACGAGA 4801

Qy 4386 TCCTGCCGTCGGGCATGCGGCCTTGAGCCTGGCGAACAGTTCGGCTGCGCGGCGAGCCCC 4445
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Db 4922 CGCTCGATGCGGATGTTTCGGCTTGGTGGTCGAATGGGCAGTAGCCGGATCAAGCGTATGC 4981

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Db 4982 AGCCGCGCATTGCATCAGCCATGATGGATACTTTCTCGGCAGGAGCCAAGGTGAGATGAC 5041

Qy 4626 AGGAGATCCTGCCCCGGCACTTCGCCCAATAGCAGCCAGTCCCTTCCCGCTTCAGTGACA 4685
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Db 5042 AGGAGATCCTGCCCCGGCACTTCGCCCAATAGCAGCCAGTCCCTTCCCGCTTCAGTGACA 5101

Qy 4686 ACGTCGAGCACAGCTGCGCAAGGAACGCCCGTCGTGGCCAGCCACGATAGCCGGCGCTGCC 4745
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Db 5102 ACGTCGAGCACAGCTGCGCAAGGAACGCCCGTCGTGGCCAGCCACGATAGCCGGCGCTGCC 5161

Qy 4746 TCGTCCTGCAGTTCATTCAGGGCACCGGACAGGTCGGTCTTGACAAAAAGAACCGGGCGC 4805
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Db 5162 TCGTCCTGCAGTTCATTCAGGGCACCGGACAGGTCGGTCTTGACAAAAAGAACCGGGCGC 5221

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Db 5222 CCCTGCGCTGACAGCCGGAACACGGCGGCATCAGAGCAGCCGATTGTCTGTTGTGCCCAG 5281

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Db 5342 TCAATCATGCGAAACGATCCTCATCCTGTCTCTTGATCAGATCTTGATCCCCTGCGCCAT 5401

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Db 5402 CAGATCCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTGCAGGGCTTCCCAACCTTACCA 5461

Qy 5046 GAGGGCGCCCCAGCTGGCAATTCGGTTCGCTTGCTGTCCATAAAACCGCCCAGTCTAGC 5105
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Db 5462 GAGGGCGCCCCAGCTGGCAATTCGGTTCGCTTGCTGTCCATAAAACCGCCCAGTCTAGC 5521

Qy 5106 TATCGGCCATGTAAGCCCACTGCAAGCTACCTGCTTTCTCTT 5146
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Db 5522 AACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGCTATT 5562
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RESULT 6
US-08-948-378A-7/c
; Sequence 7, Application US/08948378A
; Patent No. 6013258
; GENERAL INFORMATION:
    APPLICANT: Urban, Robert G.
    APPLICANT: Chicz, Roman M.
    APPLICANT: Collins, Edward J.

RESULT 7
US-09-169-425C-7/c
; Sequence 7, Application US/09169425C
; Patent No. 6183746
; GENERAL INFORMATION:
;   APPLICANT: Urban, Robert G.
;   APPLICANT: Chicz, Roman M.
;   APPLICANT: Collins, Edward J.
;   APPLICANT: Hedley, Mary Lynn
;   TITLE OF INVENTION: IMMUNOGENIC PEPTIDES FROM THE HPV E7
;   TITLE OF INVENTION: PROTEIN
;   NUMBER OF SEQUENCES: 33
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Fish & Richardson, P.C.
;   STREET: 225 Franklin Street
;   CITY: Boston
;   STATE: MA
;   COUNTRY: US
;   ZIP: 02110-2804
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Diskette
;   COMPUTER: IBM Compatible
;   OPERATING SYSTEM: Windows95
;   SOFTWARE: FastSEQ for Windows Version 2.0
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/169,425C
;   FILING DATE: 09-OCT-1998
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 60/061,657
;   FILING DATE: 09-OCT-1997
;   ATTORNEY/AGENT INFORMATION:

```
;  NAME: Fraser, Janis K.
;  REGISTRATION NUMBER: 34,819
;  REFERENCE/DOCKET NUMBER: 08191/004002
;  TELECOMMUNICATION INFORMATION:
;     TELEPHONE: 617-542-5070
;     TELEFAX: 617-543-8906
;     TELEX: 200154
INFORMATION FOR SEQ ID NO: 7:
;  SEQUENCE CHARACTERISTICS:
;     LENGTH: 4665 base pairs
;     TYPE: nucleic acid
;     STRANDEDNESS: double
;     TOPOLOGY: linear
;     MOLECULE TYPE: DNA
US-09-169-425C-7

Query Match    29.7%;    Score 1571.6;    DB 3;    Length 4665;
Best Local Similarity    86.3%;    Pred. No. 0;
Matches 1850;    Conservative 0;    Mismatches 114;    Indels 180;    Gaps 3;
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Qy   3068 GAGCAAAAGGCAGCAGAAAGGCCAGGAACCGTAAAAAGGCCGGCGGTTGCTGGCGTTTTCC 3127
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Db   2384 CTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGG 2325

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Db   2264 TGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATC 2205

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Qy   3668 TTGTTTGCAAGCAGCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGATCT 3727
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Db   1904 TTTCTACGGGGTCTGACGCTCAGTGGAACGAAAACTCACGTTAAGGGATTTTGGTCATGA 1845

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Qy   3841 GCATGGATGCCGCGGATAGCCGCTGCTGTTCCTGGATGCCGACGGATTTGCACTGCCGG 3900
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Qy   3901 ------------TAGAACTTCCGCGAGGTCGTCAGCCTCAGCAGAGTCAGCGAA 3946
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Qy   1604 CCCCGCGGTTTATGAACAAACGACCCAACACCGTGCGTTTATTCTGTCTTTTTATTGCCG 1545

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Qy   1544 TCATAGCGCGGTTCCTTCCGGTTGTCTCCTTCCGGTGTTTCAGTTAGCCTCCCCCTAG 1485

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Qy   1484 GGTGGGCGAAGAACTCAGCACATGAGATCCCGCGCTTGGAGATCATCCAGCCGGCGTCCC 1425

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Qy   1424 GGAAAACGATTCCGAAGCCCAACCTTTCATAGAAGGCGGCGGTGGAATCGAAATCTCGTG 1365

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Qy   1124 GCGGCCATTTTCCACCATGATATTCGGCAAGCAGGCATCGCCATGGGTCACGACGAGATC 1065

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Qy   1064 CTCGCCGTCGGGCATGCGCGCCTTGAGCCTGGCGAACAGTTCGGCTGGCGCGAGCCCCTG 1005

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Qy   944 CTCGATGCGATGTTTCGCTTGGTGGTCGAATGGGCAGGTAGCCGGATCAAGCGTATGCAG 885

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Db   4628 GAGATCCTGCCCCGGCACTTCGCCCAATAGCAGCCAGTCCCTTCCGCTTCAGTGACAAC 4687
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Qy   824 GAGATCCTGCCCCGGCACTTCGCCCAATAGCAGCCAGTCCCTTCCCGCTTCCAGTGACAAAC 765

Db   4688 GTCGAGCACAGCTGCGCAAGGAACGCCCGTCGTGGCCAGCCACGATAGCCGCGCTGCCTC 4747
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Qy   4747 GATTATCGTCACCAAAGCCGCCATCGTGCCT------------------------------ 3819
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Db    764 GTCGAGCACAGCTGCGCAAGGAACGCCCGTCGTGGCCAGCCACGATAGCGCGGCTGCCTC  705

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Db    704 GTCTTGCAGTTCATTCAGGCGAACACGGGCACCGGACAGGTCGGTCTTGACAAAAAGAACCGGGGCGCCC  645

Qy   4808 CTGCGCTGACAGCCGGAACACGGCCGGCATCAGAGCAGCCGATTGTCTGTTGTGCCCAGTC  4867
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Db    644 CTGCGCTGACAGCCGGAACACGGCGCGGCATCAGAGCAGCCGATTGTCTGTTGTGCCCAGTC  585

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Db    524 AATCATGCGAAACGATCCTCATCCTGTCTCTTGATCGATCTTTG  481
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RESULT 8

US-09-759-960-7/c

; Sequence 7, Application US/09759960

; Patent No. 6582704

; GENERAL INFORMATION:

; APPLICANT: Urban, Robert G.

; APPLICANT: Chicz, Roman M.

; APPLICANT: Collins, Edward J.

; APPLICANT: Hedley, Mary Lynn

; TITLE OF INVENTION: IMMUNOGENIC PEPTIDES FROM THE HPV E7

; TITLE OF INVENTION: PROTEIN

; NUMBER OF SEQUENCES: 33

; CORRESPONDENCE ADDRESS:

;   ADDRESSEE: Fish & Richardson, P.C.

;   STREET: 225 Franklin Street

;   CITY: Boston

;   STATE: MA

;   COUNTRY: US

;   ZIP: 02110-2804

; COMPUTER READABLE FORM:

;   MEDIUM TYPE: Diskette

;   COMPUTER: IBM Compatible

;   OPERATING SYSTEM: Windows95

;   SOFTWARE: FastSEQ for Windows Version 2.0

; CURRENT APPLICATION DATA:

;   APPLICATION NUMBER: US/09/759,960

;   FILING DATE:

; PRIOR APPLICATION DATA:

;   APPLICATION NUMBER: 09/169,425

;   FILING DATE:

; ATTORNEY/AGENT INFORMATION:

;   NAME: Fraser, Janis K.

;   REGISTRATION NUMBER: 34,819

;   REFERENCE/DOCKET NUMBER: 08191/004002

; TELECOMMUNICATION INFORMATION:

;   TELEPHONE: 617-542-5070

;   TELEFAX: 617-543-8906

;   TELEX: 200154

; INFORMATION FOR SEQ ID NO: 7:

; SEQUENCE CHARACTERISTICS:

;   LENGTH: 4665 base pairs

;   TYPE: nucleic acid

;   STRANDEDNESS: double

;   TOPOLOGY: linear

;   MOLECULE TYPE: DNA

US-09-759-960-7

Query Match   29.7%; Score 1571.6; DB 4; Length 4665;
Best Local Similarity 86.3%; Pred. No. 0;
Matches 1850; Conservative 0; Mismatches 114; Indels 180; Gaps 3;

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Qy   3008 ACTCAAAGGCCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGT  3067
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Db   2624 AATGCATGGGCCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGT  2565
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Db   3068 GAGCAAAAGGCCAGCAACAAAAGGCCAGGAACCGGTAAAAAGGCCGCGTTGCTGGCGTTTTCC  3127
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Qy   2564 GAGCAAAAGGCCAGCAACAAAAGGCCAGGAACCGGTAAAAAGGCCGCGTTGCTGGCGTTTTCC  2505

Db   3128 ATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAA  3187
          |||||||||||||||||||||||||||||||||| |||||||||||||||||||||||||
Qy   2504 ATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAA  2445

Db   3188 ACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTC  3247
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   2444 ACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTC  2385

Db   3248 CTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGG  3307
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   2384 CTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGG  2325

Db   3308 CGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGC  3367
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   2324 CGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGC  2265

Db   3368 TGGGCTGTGTGCACGAACCCCCGTTCAGCCGACCGGCGCTGCCTTATCCGGTAACTATC  3427
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   2264 TGGGCTGTGTGCACGAACCCCCGTTCAGCCGACCGGCGCTGCCTTATCCGGTAACTATC  2205

Db   3428 GTCTTGAGTCCAACCCGTAAGACACAGACTTATCGCCACTGGCAGCAGCCACTGGTAACA  3487
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   2204 GTCTTGAGTCCAACCCGTAAGACACAGACTTATCGCCACTGGCAGCAGCCACTGGTAACA  2145

Db   3488 GGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACT  3547
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Qy   2144 GGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACT  2085

Db   3548 ACGGCTACACTAGAAGAACAGTATTTGGTATCTCGCTCTGCTGAAGCCAGTTACCTTCG  3607
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Qy   2084 ACGGCTACACTAGAAGAACAGTATTTGGTATCTCGCTCTGCTGAAGCCAGTTACCTTCG  2025

Db   3608 GAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACACCCGCTGGTAGCGGTGGTTTTT  3667
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   2024 GAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACACCCGCTGGTAGCGGTGGTTTTT  1965

Db   3668 TTGTTTGCAAGCAGCAGATTACGGCGCAGAAAAAAGGATCTCAAGAAGATCCTTGATCT  3727
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1964 TTGTTTGCAAGCAGCAGATTACGGCGCAGAAAAAAGGATCTCAAGAAGATCCTTGATCT  1905

Db   3728 TTTCTACGGGGTCTGACGCTCAGTGGAACGAAAACTCACGTTAAGGGATTTTGGTCATGA  3787
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1904 TTTCTACGGGGTCTGACGCTCAGTGGAACGAAAACTCACGTTAAGGGATTTTGGTCATGA  1845

Db   3788 GATTATCGTCGACCAAAGCGGCCATCGTGCCT---------------------------  3819
          |||||||||||||||||||||||||||||||
Qy   1844 GATTATCAAAAAGGATCTTCACCTAGATCCTTTTAAATTAAAAATGAAGTTTTAAATCAA  1785

Db   3820 -----------------------------------CCCCACTCGTGCACCCGCGACGTTCGGGG  3840
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Qy   1784 TCTAAAGTATATATGAGTAACCTGAGGCTATGGCAGGCCGCTGTCTGATGCCGCATAGTTAAGCCAGCCCCGACACCGCCTG  1725

Db   3841 GCATGGATGCGCGGATAGCCGCTGCCTGTTCCTGGATGCCGACGGGATTTGCACTGCCGGG  3900
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Qy   1724 CGAGCCCTGGGCTTCACCCGAACTTGGGGGTGGGTGGGGGAAAAAGGAAGAAACGGGGG  1665

Db   3901 -------------TAGAACTTCCGCGAGGTCGTCCAGCCTCAGGCAGCAGCAGTGAACCAAC  3946
                       ||||||||||||||||||||||||||||||||||||||||||
Qy   1664 CGTATTGGCCCCAATGGGGTCTCGGTCGGGTGGGGTATCGACAGAGTGCCACGCCTGGGACCCGAA  1605

Db   3947 TCGCGGAGGGGGATCGA----------------------------------------------------  3961
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Qy   1604 CCCCGCGTTTATGAACAAACGACCCAACACCGCCTGCGTTTTATTCTGTCTTTTATTGCCG  1545

Qy   3962 ----------------------------------------------GCCCGG  3967
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Db   1544 TCATAGCGCGGTTCCTTCCGTATTGCTCCTTCCGTGTTTCAGTTAGTTAGCCTCCCCTAG  1485
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GENERAL INFORMATION:
 ; APPLICANT: NATURE TECHNOLOGY CORPORATION, ET AL.
 ; TITLE OF INVENTION: SELF-ASSEMBLING GENES, VECTORS AND USES
 ; THEREOF
 ; NUMBER OF SEQUENCES: 74
 ; CORRESPONDENCE ADDRESS:
 ;   ADDRESSEE: MUETING, RAASCH & GEBHARDT, P.A.
 ;   STREET: 119 NORTH FOURTH STREET, SUITE 203
 ;   CITY: MINNEAPOLIS
 ;   STATE: MINNESOTA
 ;   COUNTRY: USA
 ;   ZIP: 55401
 ; COMPUTER READABLE FORM:
 ;   MEDIUM TYPE: Floppy disk
 ;   COMPUTER: IBM PC compatible
 ;   OPERATING SYSTEM: PC-DOS/MS-DOS
 ;   SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ;   APPLICATION NUMBER: US/09/380,190A
 ;   FILING DATE: 26-Aug-1999
 ;   CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ;   APPLICATION NUMBER: PCT/US98/03918
 ;   FILING DATE: 28-FEB-98
 ; ATTORNEY/AGENT INFORMATION:
 ;   NAME: MUETING, ANN M.
 ;   REGISTRATION NUMBER: 33,977
 ;   REFERENCE/DOCKET NUMBER: 228.00010201
 ; TELECOMMUNICATION INFORMATION:
 ;   TELEPHONE: 612-305-1217
 ;   TELEFAX: 612-305-1228
 ; INFORMATION FOR SEQ ID NO: 26:
 ; SEQUENCE CHARACTERISTICS:
 ;   LENGTH: 4518 base pairs
 ;   TYPE: nucleic acid
 ;   STRANDEDNESS: single
 ;   TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-09-380-190A-26

Query Match   29.7%; Score 1570; DB 3; Length 4518;
Best Local Similarity   86.2%; Pred. No. 0;
Matches 1849; Conservative 0; Mismatches 115; Indels 180; Gaps 3;

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Qy   3008 ACTCAAAGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGT 3067
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db   1895 AATGCATGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGT 1954

Qy   3068 GAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCC 3127
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1955 GAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCC 2014

Qy   3128 ATAGGCTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAA 3187
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2015 ATAGGCTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAA 2074

Qy   3188 ACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTC 3247
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2075 ACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTC 2134

Qy   3248 CTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGG 3307
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2135 CTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGG 2194

Qy   3308 CGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGC 3367
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Db   2195 CGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGC 2254

Qy   3368 TGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCCGCCTTATCCGGTAACTATC 3427
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2255 TGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCCGCCTTATCCGGTAACTATC 2314
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Qy   3968 GGTGGGCGAAGAACTCCAGCATGAGATCCCCGCGCTGGAGCGATCATCCAGCGCGGTCCC 4027
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Db   1484 GGTGGGCGAAGAACTCCAGCATGAGATCCCCGCGCTGGAGCGATCATCCAGCGCGGTCCC 1425

Qy   4028 GGAAAACGATTCCGAAGCCCAACCTTTCATAGAAGGCGGCCGTGGAATCGAAATCTCGTG 4087
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Db   1424 GGAAAACGATTCCGAAGCCCAACCTTTCATAGAAGGCGGCCGTGGAATCGAAATCTCGTG 1365

Qy   4088 ATGGCAGGTTGGGCGTCGCTTGGTCATTCGAACCCCAGAGTCCCGCTCAGAAGAA 4147
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Db   1364 ATGGCAGGTTGGGCGTCGCTTGGTCATTCGAACCCCAGAGTCCCGCTCAGAAGAA 1305

Qy   4148 CTCGTCAAGAAGGCGATAGAAGGCGATGGCGTGCGAATCGGAGCGGCGATACCGTAAAG 4207
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Db   1304 CTCGTCAAGAAGGCGATAGAAGGCGATGGCGTGCGAATCGGAGCGGCGATACCGTAAAG 1245

Qy   4208 CACGAGGAAGCGGTCAGCCCATTCGCCGCCAAGCTCTTCAGCAATATCACGGGTAGCCAA 4267
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Db   1244 CACGAGGAAGCGGTCAGCCCATTCGCCGCCAAGCTCTTCAGCAATATCACGGGTAGCCAA 1185

Qy   4268 CGCTATGTCCTGATAGCGGTCCGCCACACCCAGCCGGCCACAGTCGATGAATCCAGAAAA 4327
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1184 CGCTATGTCCTGATAGCGGTCCGCCACACCCAGCCGGCCACAGTCGATGAATCCAGAAAA 1125

Qy   4328 GCGGCCATTTTCCACCATGATATTCGGCAAGCAGGCATCGCCATGGGTCACGACGAGATC 4387
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1124 GCGGCCATTTTCCACCATGATATTCGGCAAGCAGGCATCGCCATGGGTCACGACGAGATC 1065

Qy   4388 CTCGCCGTCGGGCATGCGCGCCTTGAGCCTGGCGAACAGTTCGGCTGGCGCGAGCCCCTG 4447
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1064 CTCGCCGTCGGGCATGCGCGCCTTGAGCCTGGCGAACAGTTCGGCTGGCGCGAGCCCCTG 1005

Qy   4448 ATGCTCTTCGTCCAGATCATCCTGATCGACAAGACCGGCTTCCATCCGAGTACGTGCTCG 4507
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Db   1004 ATGCTCTTCGTCCAGATCATCCTGATCGACAAGACCGGCTTCCATCCGAGTACGTGCTCG 945

Qy   4508 CTCGATGCGATGTTTCGCTTGGTGGTGTCGAATGGGCAGGTAGCCGGATCAAGCGTATGCAG 4567
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Db    944 CTCGATGCGATGTTTCGCTTGGTGGTGTCGAATGGGCAGGTAGCCGGATCAAGCGTATGCAG 885

Qy   4568 CCGCCCATTCGATCAGCCATGATGGATACTTTCTCGGCAGGAGCAAGGTGAGATGACAG 4627
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    884 CCGCCCATTCGATCAGCCATGATGGATACTTTCTCGGCAGGAGCAAGGTGAGATGACAG 825

Qy   4628 GAGATCCTGCCCCGGCACTTCGCCCAATAGCAGCCAGTCCCTTCCCGCTTCAGTGACAAC 4687
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    824 GAGATCCTGCCCCGGCACTTCGCCCAATAGCAGCCAGTCCCTTCCCGCTTCAGTGACAAC 765

Qy   4688 GTCGAGCACAGCTGCGCAAGGAACGCCCGTCGTGGCCAGCCACAGCGCGTGCCTC 4747
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Db    764 GTCGAGCACAGCTGCGCAAGGAACGCCCGTCGTGGCCAGCCACAGCGCGTGCCTC 705

Qy   4748 GTCTTGCAGTTCATTCAGGGCACCGGACAGGTCGGTCTTGACAAAAAGAACCGGGCGCCC 4807
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    704 GTCTTGCAGTTCATTCAGGGCACCGGACAGGTCGGTCTTGACAAAAAGAACCGGGCGCCC 645

Qy   4808 CTGCGCTGACAGCCGGAACACGGCCGGCATCGAGCACCTGGTGCAATCCATCTTGTTC 4867
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    644 CTGCGCTGACAGCCGGAACACGGCCGGCATCGAGCACCTGGTGCAATCCATCTTGTTC 585

Qy   4868 ATAGCCGAAATAGCCTCTCCACCCAAGCGGCCGGAGAACCTGCGTGCAATCCATCTTGTTC 4927
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    584 ATAGCCGAAATAGCCTCTCCACCCAAGCGGCCGGAGAACCTGCGTGCAATCCATCTTGTTC 525

Qy   4928 AATCATGCGAAACGATCTCATCCTTCCTCTTTGACATCAGATCTTG 4971
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Db    524 AATCATGCGAAACGATCTCATCCTTCCTCTTTGACATCAGATCTTG 481
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RESULT 9
US-09-380-190A-26
; Sequence 26, Application US/09380190A
; Patent No. 6410220

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Qy  3428 GTCTTGAGTCCAACCCGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACA 3487
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Db  2315 GTCTTGAGTCCAACCCGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACA 2374

Qy  3395 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3395 GCGGCCATTTCCACCATGATATTCGGCAAGCATCGCCATGGGTCACGACGAGATC 3454

Qy  3488 GGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACT 3547
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2375 GGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACT 2434

Qy  4388 CTCGCCGTTCGGCGATGCGCGCCCTTGAGCTGCCTTGAGCTGCCTTGGCGGCCGAAGAGTTCGGCGCCGAGCCCCTG 4447
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3455 CTCGCCGTTCGGCGATGCGCGCCCTTGAGCTGCCTTGGCGGCCGAAGAGTTCGGCGCCGAGCCCCTG 3514

Qy  3548 ACGGGCTACACTTAGAAGAACAGTATTTGTATCTGCGCTGCTGAAGCCAGTTACCTTCG 3607
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Db  2435 ACGGGCTACACTTAGAAGAACAGTATTTGTATCTGCGCTGCTGAAGCCAGTTACCTTCG 2494

Qy  4448 ATGCTCTTCGTCCAGATCATCCTGATCGACAAGACCGCTTCATCCCAGTACGTGCTCG 4507
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Db  3515 ATGCTCTTCGTCCAGATCATCCTGATCGACAAGACCGCTTCATCCCAGTACGTGCTCG 3574

Qy  3608 GAAAAAGAGTTGGTAGCTGTTCGCTTGGTCAAACAAACCACCACCCGCTGGTGGTTTTT 3667
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Db  2495 GAAAAAGAGTTGGTAGCTGTTCGCTTGGTCAAACAAACCACCACCCGCTGGTGGTTTTT 2554

Qy  4508 CTCGATGCGATGTTTCGCTTGGTCGAATGGGCAGTAGCCAGTATGCAG 4567
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Db  3575 CTCGATGCGATGTTTCGCTTGGTCGAATGGGCAGTAGCCAGTATGCAG 3634

Qy  3668 TTGTTTGCAAGCAGCAGATTAGGCGCAGAGAAGGATCTCAAGAAGATCCTTTGATCT 3727
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Db  2555 TTGTTTGCAAGCAGCAGATTACGCGCAGAGAAGGATCCTTTGATCT 2614

Qy  4568 CCGCCGCATTGCATCAGCCATGATGGATACTTTCTCGGCAGGAGCAAGTGAGATGACAG 4627
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3635 CCGCCGCATTGCATCAGCCATGATGGATACTTTCTCGGCAGGAGCAAGTGAGATGACAG 3694

Qy  3728 TTTCTACGGGTCTGACGCTCAGTGGAACGAAAACTCACGTTAAGGGATTTTGGTCATGA 3787
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Db  2615 TTTCTACGGGTCTGACGCTCAGTGGAACGAAAACTCACGTTAAGGGATTTTGGTCATGA 2674

Qy  4628 GAGATCCTGCCCCGGCACTTCGCCAATAGCAGCCAGTCCCTTCCCGCTTCCAGTGACAAC 4687
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3695 GAGATCCTGCCCCGGCACTTCGCCAATAGCAGCCAGTCCCTTCCCGCTTCCAGTGACAAC 3754

Qy  3788 GATTATCGTCGACCAAAGCGGCCATCGTGCCT 3819
         ||||||
Db  2675 GATTATCAAAAAGGATCTTCACCTAGATCCTTTTAAATTAAAAATGAAGTTTTAAATCAA 2734

Qy  4688 GTCGAGCAGCAGCAGTGCGCAAGGAACGCCCGTCGTGGCCAGCCACGATAGCCGCTGCCTC 4747
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3755 GTCGAGCAGCAGCAGTGCGCAAGGAACGCCCGTCGTGGCCAGCCACGATAGCCGCTGCCTC 3814

Qy  3820 CCCCACTTCCTGCAGTTCGGGG 3840
               ||||||||||||||||||
Db  2735 TCTAAAGTATATATGAGTAACCTGAGGCTATGCGAGGGCCTGCGCCCGACGTTGCCTG 2794

Qy  4748 GTCCTGCAGTTCATTCAGGCGCACCGGACAGGTCGGTCTTGACAAAAGAACCCGGGCGCCC 4807
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3815 GTCTTGCAGTTCATTCAGGCGCACCGGACAGGTCGGTCTTGACAAAAGAACCGGGCGCCC 3874

Qy  3841 GCATGGATGCGGGATAGCGCCGCTGCTGTTTCCTGATGCCGACGATTTGCACTGCCGCGG 3900
         ||||||||||||||||||||||| |||  ||  |
Db  2795 CGAGCCCCTGGGCCTTCACCCGAACTTGGGGGTGGGGAAAAGGAGAAACGCGGG 2854

Qy  4808 CTGCGCTGACAGCGGAACACGGCGGCGATCAGAGCAGCGGCGGATTGTCTGTTGCCCAGTC 4867
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3875 CTGCGCTGACAGCGGAACACGGCGGCGATCAGAGCAGCGGCGGATTGTCTGTTGTGTCCCAGTC 3934

Qy  3901 TAGAACTCCGCGAGTTCCTCCAGCCTCAGGCAGCAGCTGAACCAAC 3946
              |||  ||   ||  || || | |
Db  2855 CGTATTGGCCCCAATGGGGTCTCGGTGGGGTATCGACAGAGTGCCAGCCCGGGACCGAA 2914

Qy  4868 ATAGCCGAATAGCCTCTCCACCCAAGCGGCCGGAGAACCTGCGTGCAATCCATCATCTTGTTC 4927
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3935 ATAGCCGAATAGCCTCTCCACCCAAGCGGCCGGAGAACCTGCGTGCAATCCATCATCTTGTTC 3994

Qy  3947 TCGCGAGGGGATCGA 3961
              ||
Db  2915 CCCGCGGTTTATGAACAAACGACCCAACACCCGCGTTTATTCTGTCTTTTTATTGCCG 2974

Qy  4928 AATCATGCGAAACGATCCTCATCCTGTCTCTTGATCAGATCTTG 4971
         |||||||||||||||||||||||||||| |||
Db  3995 AATCATGCGAAACGATCCTCATCCTGTCTCTTGATCGATCTTTG 4038

Qy  3962 ----------------------------------GCCCGG 3967
                                           ||
Db  2975 TCATAGCGCGGGTTCCTTCCGTATTGTCTCCTTCCGTGTTTCAGTTAGCCTCCCCTAG 3034

Qy  3968 GGTGGGCGAAGAACTCCAGCATGAGATCCCGCGCTGGAGGATCATCCAGCCAGCCGCTCCC 4027
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3035 GGTGGGCGAAGAACTCCAGCATGAGATCCCGCGCTGGAGGATCATCCAGCCAGCCGCTCCC 3094

Qy  4028 GAAAAACGATTCCGAAGCCCAACCTTTCATAGAAGGCGGCCGTGAATCGAAATCTCGTG 4087
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3095 GAAAAACGATTCCGAAGCCCAACCTTTCATAGAAGGCGGCCGTGAATCGAAATCTCGTG 3154

Qy  4088 ATGGCAGGTTGGGCGTCGCTGGTCGGTCATTTGAACCCCAGAGTTCCCCGCTCAGAAGAA 4147
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Db  3155 ATGGCAGGTTGGGCGTCGCTGGTCGGTCATTTGAACCCCAGAGTTCCCCGCTCAGAAGAA 3214

Qy  4148 CTCGTCAAGAAGGCGATAGAGGCCGATGCGCTGGAATCGGCCGCGATACCGGTAAAG 4207
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Db  3215 CTCGTCAAGAAGGCGATAGAGGCCGATGCGCTGGAATCGGCCGCGATACCGGTAAAG 3274

Qy  4208 CACGAGGAAGCGGTCAGCCATTCGCCGCCAAGCTCTTCAGCAATATCACGGGTAGCCAA 4267
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3275 CACGAGGAAGCGGTCAGCCATTCGCCGCCAAGCTCTTCAGCAATATCACGGGTAGCCAA 3334

Qy  4268 CGCTATGTCCTGATAGCGGTCGATGAATCCAGTCGATGAATCCAGAAAAA 4327
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Db  3335 CGCTATGTCCTGATAGCGGTCGATGAATCCAGTCGATGAATCCAGAAAAA 3394

Qy  4328 GCGGCCATTTTCCACCATGATATTCGGCAAGCAGGCATCGCCATGGGTCACGACGAGATC 4387
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Db  4295 AATGCATGGCGTAATACGTTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGT 4236
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RESULT 10
US-09-533-220A-4/c
; Sequence 4, Application US/09533220A
; Patent No. 6406908
; GENERAL INFORMATION:
; APPLICANT: Mcintyre, Peter
; APPLICANT: James, Iain Fraser
; TITLE OF INVENTION: Human Vanilloid Receptor
; FILE REFERENCE: 4-30875A
; CURRENT APPLICATION NUMBER: US/09/533,220A
; CURRENT FILING DATE: 2000-03-23
; PRIOR APPLICATION NUMBER: UNITED KINGDOM 9907097.1
; PRIOR FILING DATE: 1999-03-26
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 1.30
; SEQ ID NO 4
; LENGTH: 4886
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-533-220A-4

Query Match   29.7%; Score 1570; DB 3; Length 4886;
Best Local Similarity 86.2%; Pred. No. 0;
Matches 1849; Conservative   0; Mismatches 115; Indels 180; Gaps   3;

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Qy  3008 ACTCAAAGGCGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGT 3067
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Db  4295 AATGCATGGCGTAATACGTTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGT 4236
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Qy  3068 GAGCAAAAGGCCAGCAAGAACCGCTAAAAAGGCCGCGTTGCTGCGCGTTTTTCC 3127
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Db  4235 GAGCAAAAGGCCAGCAAGAACCGCTAAAAAGGCCGCGTTGCTGCGCGTTTTTCC 4176

Qy  3155 GGTGGGCGGAAGAACTCCAGCATGAGATCCCGCGTGGAGGATCATCCAGCCGGCGTCCC 3096
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Db  3128 ATAGGCTCCGCCCCCTGACGAGCTCACAAAAATCGACGCTCAAGTCAGAGGTCGGCGAA 3187
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Db  4028 GGAAAACGATTCCGAGCCCAACCTTTCATAGAGAAGGCGGCGGTGGAATCGAAATCTCGTG 4087

Qy  3175 ATAGGCTCCGCCCCCTGACGAGCTCACAGAGCTCAGAGGTCGGCGAA 4116
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Qy  3248 CTGTTCCGACCCTGCCGCTTACCGGATACCGTTCCGCCCTTTCTCCCCTGGGAAGCGTGG 3307

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Db  3395 CGAGCCCTGGGCCTTCACCCCGAACTTGGGGGTGGGGAAAAGGAAGAAACCGCGGG 3336

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Qy  3947 TCGCGAGGGGATCGA-------- 3961

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Qy  3962 --------GCCCGG 3967

Db  3155 GGTGGGCGGAAGAACTCCAGCATGAGGATCATCCAGCCGGCGTCCC 3968
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RESULT 11
US-08-751-767A-7/c
; Sequence 7, Application US/08751767A
; Patent No. 5594104
; GENERAL INFORMATION:

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APPLICANT: ANDERSON, ROBERT J.
APPLICANT: GRANT, HUGH
APPLICANT: MACDONALD, IAN D.
TITLE OF INVENTION: INTERLEUKIN-12 FUSION PROTEIN
NUMBER OF SEQUENCES: 80
CORRESPONDENCE ADDRESS:
  ADDRESSEE: NIXON & VANDERHYE P.C.
  STREET: 1100 NORTH GLEBE ROAD
  CITY: ARLINGTON
  STATE: VA
  COUNTRY: USA
  ZIP: 22201
COMPUTER READABLE FORM:
  MEDIUM TYPE: Floppy disk
  COMPUTER: IBM PC compatible
  OPERATING SYSTEM: PC-DOS/MS-DOS
  SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/08/751,767A
  FILING DATE: 08-NOV-1996
  CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
  NAME: SADOFF, B.J.
  REGISTRATION NUMBER: 36,663
  REFERENCE/DOCKET NUMBER: 117-221
TELECOMMUNICATION INFORMATION:
  TELEPHONE: 7038164091
  TELEFAX: 7038164100
INFORMATION FOR SEQ ID NO: 7:
  SEQUENCE CHARACTERISTICS:
    LENGTH: 6139 base pairs
    TYPE: nucleic acid
    STRANDEDNESS: both
    TOPOLOGY: linear
  MOLECULE TYPE: cDNA
  FEATURE:
    NAME/KEY: CDS
    LOCATION: 3222..4841
US-08-751-767A-7
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Query Match          29.7%;   Score 1570;  DB 2;  Length 6139;
Best Local Similarity 86.2%;  Pred. No. 0;
Matches 1849;  Conservative 0;  Mismatches 115;  Indels 180;  Gaps 3;

Qy  3008 ACTCAAAGGCGGTAATACGGTTATCATCCAGAATCAGGGGATAACGCAGGAAAGAACACATGT 3067
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Qy  3068 GAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCC 3127
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Db  2564 GAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCC 2505

Qy  3128 ATAGGCTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAA 3187
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Qy  3188 ACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTC 3247
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Qy  3248 CTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGG 3307
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Db  2384 CTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGG 2325

Qy  3308 CGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGC 3367
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Db  2324 CGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGC 2265

Qy  3368 TGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATC 3427
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Db  2264 TGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATC 2205

Qy  3428 GTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACA 3487
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Db  2204 GTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACA 2145

Qy  3488 GGATTAGCAGAGCGAGCGAGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACT 3547
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Db  2144 GGATTAGCAGAGCGAGCGAGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACT 2085

Qy  3548 ACGGCTACACTAGAAGAACAGTATTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCG 3607
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Db  2084 ACGGCTACACTAGAAGGACAGTATTCGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCG 2025

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Qy  3728 TTTCTACGGGGTCTGACGCTCAGTGGAACGAAAACTCACGTTAAGGGATTTTTGGTCATGA 3787
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Db  1904 TTTCTACGGGGTCTGACGCTCAGTGGAACGAAAACTCACGTTAAGGGATTTTTCGTCATCA 1845

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Db  1844 GATTATCAAAAAGGATCTTCACCTAGATCCTTTAAATTAAAAATGAAGTTTTAAATCAA 1785

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Qy  3947 TCGCGAGGGGATCGA---------------------- 3961
                                                   
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Qy  3962 --------------GCCCGG 3967
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Db  1544 TCATAGCGCGGTTCCTTCCGTATTGTCTCCTTCCGTGTTTCAGTTAGCCTCCCGGCTCCC 1485

Qy  3968 GGTGGGCGAAGAACTTCCAGCATGAGAATCCCGCGTTGCTGGAGGATCATCCAGCCGGTTTTTCC 4027
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Db  1484 GGTGGGCGAAGAACTTCCAGCATGAGAATCCCGCGTTGCTGGAGGATCATCCAGCCGGTTTTTCC 1425

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Qy  4088 ATGGCAGGTTGGGCGTCGCTTGGTCGGTTCGGTCATTTGCAACCCGAGTCCCGCTCAGAAGAA 4147
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Qy  4448  ATGCTCTTCCTCGTCCAGATCATCCTGATCGACAAGACCGGCTTCCATCCGAGTACGTGCTCG  4507       Db  4624  CTCCGCCCCCTGACGAGCATCACAAAAATCGAGCGTCAAGTCAGGAGGTGGCGAACCCG  4565
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Qy  4748  GTCCTTGCAGTTCATTCAGGGGACCGACCAGTCCGGTCTTCTTGACAAAAGAACCGGGCGCCC  4807       Db  4324  GAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCACTGGTAACACGGATT  4265
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Qy  4928  AATCATGCGAAACGATCCTCATCCTGTCTCTTGATCAGATCTTG  4971       Db  4144  AGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGTGAGCGGTGGTTGTTTTTTGTT  4085
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RESULT 12                                                                       Qy  3733  ACGGGGTTCTGACGCTCAGTGGAACGAAAACTCACGTTAAGGGATTTTGGTCATGAGATTA  3792
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; Patent No. 6632671                                                            Db  3793  TCGTCGACCAAAGCGGCCATCGTGCCT----  ...
; GENERAL INFORMATION:                                                          Db  3964  TCAAAAAGGATCTTCACCTAGATCCTTTAAATTAAAAATGAAGTTTAAATCAATCTAA  3905
;   APPLICANT: Genegesgues, Inc.                                                Qy  3820  -------------CCCACTCCTGCAGTTCGGGGCATG  3845
;   TITLE OF INVENTION: NANOCAPSULE ENCAPSULATION SYSTEM AND METHOD             Db  3904  AGTATATATGAGTAACCTGAGGCTATGGCAGGGCCTGCCGCCGACGTTGGCTGCGAGC  3845
;   FILE REFERENCE: G332.12-0001                                               Qy  3846  GATGCGCGGATAGCCCGCTGCTGGTTTCCTGGATGCGCGGACGATTTGCACTGCCGG----  3900
;   CURRENT APPLICATION NUMBER: US/09/796,575                                  Db  3844  CCTGGGCCTTCACCCGAACTTGGGGGTGGGGGAAAAGGAAAGAAAACGCGGGCGTAT  3785
;   CURRENT FILING DATE: 2001-02-28                                            Qy  3901  -------TAGAACTCCGGCGAGTTCGTCGAGCTTCGCG  3951
;   PRIOR APPLICATION NUMBER: US 60/185,282                                    Db  3784  TGGCCCCAATGGGGTCTCGGTGGGGTATCGACAGAGTGCCACGCCCTGGGACCGAACCCCG  3725
;   PRIOR FILING DATE: 2000-02-28                                              Qy  3952  AGGGGGATCGA-  3961
; NUMBER OF SEQ ID NOS: 5                                                       Db  3724  CGTTTATGAACAAACGACCCAACACCGTGCGTTTTTATTCTGTCTTTTATTGCCGTCATA  3665
; SEQ ID NO 4                                                                  Qy  3962  -------------GCCCGGGGTGG  3972
;   LENGTH: 4748                                                               Db  3664  GCGCGGGTTCCTTCCGTATTGTCTTCCGTGTTTCAGTTAGCCTCCCCCTAGGGTGG  3605
;   TYPE: DNA                                                                  Qy  3973  GCGAAGAACTCCAGCATGAGATCCCCGCGCTGGAGGATCATCCAGCCGGCGTCCCGGAAA  4032
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Provided by Dr. Brett Levay-Young of the University of Minnesota
US-09-796-575-4

Query Match      29.7%;  Score 1569.8;  DB 4;  Length 4748;
Best Local Similarity   86.3%;  Pred. No. 0;
Matches  1847;  Conservative     0;  Mismatches   112;  Indels  180;  Gaps      3;

Qy  3013  AAGGGCCGTAATACGGTTATCCACAGAATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCA  3072
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Db  4744  ATGGGCCGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCA  4685
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APPLICANT: Genesegues, Inc.
; TITLE OF INVENTION: NANOCAPSULE ENCAPSULATION SYSTEM AND METHOD
; FILE REFERENCE: G332.12-0001
; CURRENT APPLICATION NUMBER: US/09/796,575
; CURRENT FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: US 60/185,282
; PRIOR FILING DATE: 2000-02-28
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 4992
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Supplied by BD Biosciences Clonetech of Palo Alto, California
US-09-796-575-5

Query Match   29.7%; Score 1569.8; DB 4; Length 4992;
Best Local Similarity 86.3%; Pred. No. 0;
Matches 1847; Mismatches 112; Conservative 0; Indels 180; Gaps 3;

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Qy    3013 AAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCA 3072
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Db    4988 ATGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCA 4929

Qy    3073 AAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGG 3132
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4928 AAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGG 4869

Qy    3133 CTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCG 3192
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4868 CTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCG 4809

Qy    3193 ACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTT 3252
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Db    4808 ACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTT 4749

Qy    3253 CCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTT 3312
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4748 CCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTT 4689

Qy    3313 TCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGC 3372
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Db    4688 TCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGC 4629

Qy    3373 TGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTT 3432
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Db    4628 TGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTT 4569

Qy    3433 GAGTCCAACCCGGTAAGACAGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATT 3492
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Db    4568 GAGTCCAACCCGGTAAGACAGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATT 4509

Qy    3493 AGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCGCTAACTACGCGC 3552
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Db    4508 AGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCGCTAACTACGCGC 4449

Qy    3553 TACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAA 3612
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Db    4448 TACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAA 4389

Qy    3613 AGAGTTGGTAGCTCTTGATCCGGCAAACAACAACCACCGCTGGTAGCGGTGGTTTTTTGTT 3672
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Db    4388 AGAGTTGGTAGCTCTTGATCCGGCAAACAACAACCACCGCTGGTAGCGGTGGTTTTTTGTT 4329

Qy    3673 TGCAAGCAGCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCT 3732
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Db    4328 TGCAAGCAGCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCT 4269

Qy    3733 ACGGGGTCTGACGCTCAGTGGAACGAAAACTCACGTTAAGGGATTTTGGTCATGAGATTA 3792
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Db    4268 ACGGGGTCTGACGCTCAGTGGAACGAAAACTCACGTTAAGGGATTTTGGTCATGAGATTA 4209
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Db    3604 GGAAGAGACTCCAGCAGATGAGAGATCCCCGCGCTGAGGATCATCCAGCCGCCGTCCCCGAAA 3545
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Qy    4033 ACGATTCCGAAGCCCAACCTTTCATACGAAGACGGCGGTGGAATCGAAATCTCGTGATGGC 4092
           |||||||||||||| ||||||||||||||||||||
Db    3544 ACGATTCCGAAGCCCAACCTTTCATACGAAGACGGCGGTGGAATCGAAATCTCGTGATGGC 3485

Qy    4093 AGGTTGGGCGTCGTCATTTCGGTCATTGGAACCCCAGAGTCCGCTCAGAAGAACTCGT 4152
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Db    3484 AGGTTGGGCGTCGTCATTTCGGTCATTGGAACCCCAGAGTCCGCTCAGAAGAACTCGT 3425

Qy    4153 CAAGAAGGCGATAGAAGGCGATGCGCTGCGAATCGGGAGCGGCGATACCGTAAAGCACGA 4212
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Db    3424 CAAGAAGGCGATAGAAGGCGATGCGCTGCGAATCGGGAGCGGCGATACCGTAAAGCACGA 3365

Qy    4213 GGAAGCGGTCAGCCCATTCGCCGCCAAGCTCTTCAGCAATATCACGGGTAGCCAACGCTA 4272
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Db    3364 GGAAGCGGTCAGCCCATTCGCCGCCAAGCTCTTCAGCAATATCACGGGTAGCCAACGCTA 3305

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Db    3304 TGTCCTGATAGCGGTCCGGCCACACCCAGCCGGCCACACCCAGCCGGCCACAGTCGAATGAATCCGGC 3245

Qy    4333 CATTTTCCACCATGATATTCGGCAAGCAGGCATCGCCATGGGTCACGACGAGATCCTCGC 4392
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Qy    4393 CGTCGGGCATGCGCGCCTTGAGCCTGGCGAACAGTTCGGCTGGCGCGAGCCCCTGATGCT 4452
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Qy    4453 CTTCGTGTCCAGATCATCCTGATGACAAGACCGGCTTCCATCCGAGTACGTGCTCGCTCGA 4512
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Db    3124 CTTCGTGTCCAGATCATCCTGATGACAAGACCGGCTTCCATCCGAGTACGTGCTCGCTCGA 3065

Qy    4513 TGCGGATGTTTCGCTTGGTGGTCGAATGGGCAGGTAGCCGGATCAAGCGTATGCAGCCGCC 4572
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Db    3064 TGCGGATGTTTCGCTTGGTGGTCGAATGGGCAGGTAGCCGGATCAAGCGTATGCAGCCGCC 3005

Qy    4573 GCATTGCATCAGCCATGATGGATACTTTCTCGGCAGAGCAAGGTGAGATGACAGAGGAGAT 4632
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Db    3004 GCATTGCATCAGCCATGATGGATACTTTCTCGGCAGAGCAAGGTGAGATGACAGAGGAGAT 2945

Qy    4633 CCTGCCCCGGCACTTCGCCCAATAGCAGCCAGTCCCTTCCCGCTTCCCGTGACCAACGTCGA 4692
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Db    2944 CCTGCCCCGGCACTTCGCCCAATAGCAGCCAGTCCCTTCCCGCTTCCCGTGACCAACGTCGA 2885

Qy    4693 GCACAGCTGCGCAAGGAACGCCCGTCGTGGCCAGCCACGATAGCCGCGCTGCCTGCGTCCT 4752
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Db    2884 GCACAGCTGCGCAAGGAACGCCCGTCGTGGCCAGCCACGATAGCCGCGCTGCCTGCGTCTT 2825

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Db    2824 GCAGTTCATTCAGGGCACCGGACACCGGACAGTTCGGTCGTCTTGACAAAAAGAACCGGGGCGCCCTGCG 2765

Qy    4813 CTGACAGCCGGAACACGGCGGCATCAGAGCAGCCGATTGTCTGTTGTGCCCAGTCATAGC 4872
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Db    2764 CTGACAGCCGGAACACGGCGGCATCAGAGCAGCCGATTGTCTGTTGTGCCCAGTCATAGC 2705

Qy    4873 CGAATAGCCTCTCCACCCAAGCGGCCGGAGAACCTGCGTGCAATCCATCTTGTTCAATCA 4932
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Db    2704 CGAATAGCCTCTCCACCCAAGCGGCCGGAGAACCTGCGTGCAATCCATCTTGTTCAATCA 2645

Qy    4933 TGCGAAACGATCCTCATCCTGTCTCTTGATCAGATCTTG 4971
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Db    2644 TGCGAAACGATCCTCATCCTGTCTCTTGATCGATCTTG 2606
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RESULT 13
US-09-796-575-5/c
; Sequence 5, Application US/09796575
; Patent No. 6632671
; GENERAL INFORMATION:

RESULT 14
US-09-393-483A-1/c
; Sequence 1, Application US/09393483A
; Patent No. 6689936
; GENERAL INFORMATION:
;   APPLICANT: Burgeson, Robert
;   APPLICANT: Amano, Satoshi
;   APPLICANT: Kishimoto, Jiro
;   APPLICANT: Nishiyama, Toshio
;   APPLICANT: Ehana, Ritsuko
;   TITLE OF INVENTION: METHODS FOR EVALUATING A COMPOUND FOR
;   TITLE OF INVENTION: ITS EFFECT ON SKIN
;   FILE REFERENCE: 10287-054001
;   CURRENT APPLICATION NUMBER: US/09/393,483A
;   CURRENT FILING DATE: 1999-09-10
;   PRIOR APPLICATION NUMBER: 09/070,436
;   PRIOR FILING DATE: 1998-04-30
;   PRIOR APPLICATION NUMBER: 60/069,945
;   PRIOR FILING DATE: 1997-12-17
;   NUMBER OF SEQ ID NOS: 7
;   SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 5069
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-393-483A-1

Query Match   29.7%;   Score 1569.8;   DB 4;   Length 5069;
Best Local Similarity 86.3%;   Pred. No. 0;
Matches 1847; Conservative 0; Mismatches 112; Indels 180; Gaps 3;

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Db 4765 TCTCATAGCTCACGCTGTAGGTATCTCAGTTCGTGTGTAGGTCGTTCGGTGTGGCTCGTGCTCCAAGCTGGGC 4706

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Qy 3433 GAGTCCAACCCGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATT 3492
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Db 4585 AGCAGAGCCGAGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGC 4526

Qy 3553 TACACTAGAAGAACAGTATTTGTATCTGCGCTCGCTGCTGAAGCCAGTTACCTTCGGAAAA 3612
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Db 4525 TACACTAGAAGAACAGTATTTGTATCTGCGCTCGCTGCTGAAGCCAGTTACCTTCGGAAAA 4466

Qy 3613 AGAGTTGGTAGCTCTTGATCCGGCAAACAACCACCGCTGTAGCCGTGGTGGTTTTTTTGTT 3672
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Db 4465 AGAGTTGGTAGCTCTTGATCCGGCAAACAAACACCGCTGTAGCCGTGGTGGTTTTTTTGTT 4406

Qy 3673 TGCAAGCAGCAGATTACGACGGCGTGCTCAGTGAACGAAAACTCAAGAAGATCCTTCTTTCT 3732
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Db 4405 TGCAAGCAGCAGATTACGACGGCGTGCTCAGTGGAACGAAAACTCAAGAAGATCCTTCTTTCT 4346

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Qy 3793 TCGTCGACCAAAGCGGCCATCGTGCCT------- 3819
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Db 4285 TCAAAAGGATCTTCACCTAGATCCTTTTAAATTAAAAATGAAGTTTAAATCAATCTAA 4226

Qy 3820 ------- CCCACTCCTGCAGTTCGGGGGCATG 3845
Db ------- CCCACTCCTGCAGTTCGGGGGCATG

Qy 4225 AGTATATATGAGTAACCTGAGGCTATGCGAGGGCCTGCGCCCGACGTTGGCTGCGAGC 4166
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Qy 3846 GATGCGCGGATAGCCGCTGCTGGTTTCCTGATGCGACGGATTTGCACTGCCG------- 3900
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Db 4165 CCTGGGCCTTCACCCGGAACTTGGGGGGTGGGGTGGGGGAAAAACGCGGGGCGTAT 4106

Qy 3901 -------TAGAACTCCGCGGAGGTCGTCCAGCCTCAGCCGCAGCAGCTGAACCAACTCGCG 3951
                |||   |  | |||||| |
Db 4105 TGGCCCCAATGGGGTCTCGGTGGGGTATCGACAGAGTGCCCTGGGGACCGGAACCCCG 4046

Qy 3952 AGGGGATCGA------- 3961
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Qy 3962 -------GCCCGGGGGTGG 3972
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Db 3985 GCGCGGGGGTTCCTTCCCGTATTGTCTCCTTCCCGCGCTGGAGGATCATCCAGCCGGTCCCCGGCGTCCCCGGAA 3926

Qy 3973 GCGAAGAAACTCCAGCAGCATGAGAATCCCCGCGCTGAGGATCATCCAGCCGGTCCCCGGAAA 4032
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Db 3925 GCGAAGAAACTCCAGCAGCATCCAGCCGTGAGGATCATCCAGCCGGTCCCCGGAAA 3866

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Db 3865 ACGATTCCGAAGCCCAACCTTTCATAGAAGGCGGCCGGTGAATCGAAATCTCGTGATGGC 3806

Qy 4093 AGGTTGGGCGTCGCGTTGGTCGGTCATTTGGTCGGTCATTTCGAACCCGCTCAGAGAACTCGT 4152
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Db 3745 CAAGAAGGCGATAGAAGGCCGATGCGCTGCGAATCGGGAGCCGGCGGATACCGTAAAGCACGA 3686

Qy 4213 GGAAGCGGTCAGCCCATTCGCCGCCAAGCTCTTCAGCAATATCACGGGTAGCCAACGCTA 4272
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Db 3685 GGAAGCGGTCAGCCCATTCGCCGCCAAGCTCTTCAGCAATATCACGGGTAGCCAACGCTA 3626
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Qy 4273 TGTCCTGATAGGCGTCCGGCCACACCCAGCCGCCGGCCACAGTGTCGATGAATCCAGAAAAGCGGC 4332
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Db 3625 TGTCCTGATAGGCGTCCGGCCACACCCAGCCGCCGGCCACAGTGTCGATGAATCCAGAAAAGCGGC 3566

Qy 4333 CATTTTCACCATGATATTCGGCAAGCAGCATCGCCATGGGTCACGACGAGATCCTCGC 4392
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Qy 4393 CGTCGGCATGGCGCCTTGAGCCTTGCGAACAGTTCGGCTGCGCGGAGCCCCTGATGCT 4452
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Db 3505 CGTCGGGCATGCGCCTTGAGCCTTGCGGGCTGCGGGCAGTTCGGCTGCGCGGAGCCCCTGATGCT 3446

Qy 4453 CTTCGTCCAGATCATCCTGATCGACAAGACCGGCTTCCATCCGAGTACGGCTTCGCTGA 4512
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Db 3445 CTTCGTCCAGATCATCCTGATCGACAAGACCGGCTTCCATCCGAGTACGGCTTCGCTCGA 3386

Qy 4513 TGCGAGTGTTCGGTCGGTGGTGAATGGCAGGCAGTAGCCGGATCAAGCGTATGCAGCCGCC 4572
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Db 3385 TGCGAGTGTTCGGTCGGTGGTGAATGGCAGGCAGTAGCCGGATCAAGCGTATGCAGCCGCC 3326

Qy 4573 GCATTGCATCAGCCATGATGATACTTTCTCGGCAGGAGCAAGTGAGATGACAGGAGAT 4632
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Db 3325 GCATTGCATCAGCCATGATGATACTTTCTCGGCAGGAGCAAGTGAGATGACAGGAGAT 3266

Qy 4633 CCTGCCCCGGCACTTCGCCCAATAGCAGCCAGTCCCTTCCCGCTTCCAGTGACAACGTCGA 4692
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Db 3265 CCTGCCCCGGCACTTCGCCCAATAGCAGCCAGTCCCTTCCCGCTTCCAGTGACAACGTCGA 3206

Qy 4693 GCACAGCTGCGCAAGGAACGCCCGTCGTGGCCAGCCACGATAGCCGCGCTGCCTCGTCCT 4752
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Db 3205 GCACAGCTGCGCAAGGAACGCCCGTCGTGGCCAGCCACGATAGCCGCGCTGCCTCGTCTT 3146

Qy 4753 GCAGTTCATTCAGGGCACCGGACAGTCGGTTCGTCTTGACAAAAGAACCGGGCCCCCGCG 4812
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Db 3145 GCAGTTCATTCAGGGCACCGGACAGTCGGTTCGTCTTGACAAAAGAACCGGGCCCCCTCG 3086

Qy 4813 CTGACAGCCGGAACACGGCGCGCATCAGAGCAGCAGCCGATTGTCTGTTGTCCCAGTCATAGC 4872
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Db 3085 CTGACAGCCGGAACACGGCGCGCATCAGAGCAGCAGCCGATTGTCTGTTGTCCCAGTCATAGC 3026

Qy 4873 CGAATAGCCTCTCCACCCAAGCGGCGCCGGAGAACCTGCGTGCAATCCATCTTCGTTCAATCA 4932
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Db 3025 CGAATAGCCTCTCCACCCAAGCGGCGCCGGAGAACCTGCGTGCAATCCATCTTCGTTCAATCA 2966

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Db 2965 TGCGAAACGATCCTCATCCTCGTCCTCTTGATCGATCTTG 2927
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;  TYPE: DNA
;  ORGANISM: Homo sapiens
US-09-393-483A-2

Query Match        29.7%;  Score 1569.8;  DB 4;  Length 5069;
Best Local Similarity  86.3%;  Pred. No. 0;
Matches 1847;  Conservative  0;  Mismatches  112;  Indels  180;  Gaps  3;
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Qy   3073 AAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGGTTGTGCGGTTTTTCCATAGG 3132
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Db     65 AAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGGTTGTGCGGTTTTTCCATAGG 124

Qy   3133 CTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCG 3192
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Db    125 CTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCG 184

Qy   3193 ACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTT 3252
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Db    185 ACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTT 244

Qy   3253 CCGACCCTGCGCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTT 3312
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Db    245 CCGACCCTGCGCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTT 304

Qy   3313 TCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGC 3372
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Db    305 TCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGC 364

Qy   3373 TGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTT 3432
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    365 TGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTT 424

Qy   3433 GAGTCCAACCCGGTAAGACATACGACTTATCGGCAGCAGCCACTGGTAACAGGATT 3492
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Db    425 GAGTCCAACCCGGTAAGACACTTATCGGCAGCAGCCACTGGTAACAGGATT 484

Qy   3493 AGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGTGGCCTAACTACGGC 3552
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Db    485 AGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGTGGCCTAACTACGGC 544

Qy   3553 TACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCCGAAAA 3612
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                    GenCore version 5.1.6

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OM nucleic - nucleic search, using sw model

Run on:      July 3, 2005, 00:29:22 ; Search time 2895 Seconds
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Title:       US-09-921-143-36
Perfect score: 5283
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Scoring table: IDENTITY_NUC
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Searched:    6313374 seqs, 3136092125 residues

Total number of hits satisfying chosen parameters:    12626748

Minimum DB seq length: 0
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	2240	42.4	8349	16	US-10-198-478-16	Sequence 16, Appl
3	2240	42.4	11546	20	US-10-841-796-33	Sequence 33, Appl
c 4	1793.4	33.9	4800	16	US-10-322-360-1	Sequence 1, Appli
5	1697.8	32.1	4058	21	US-10-811-028A-5	Sequence 5, Appli
6	1697.8	32.1	4187	21	US-10-811-028A-6	Sequence 6, Appli
7	1697.8	32.1	4293	21	US-10-811-028A-2	Sequence 2, Appli

8	1697.8	32.1	4332	21	US-10-811-028A-1	Sequence 1, Appli
9	1697.8	32.1	5753	21	US-10-811-028A-3	Sequence 3, Appli
10	1697.8	32.1	5760	21	US-10-811-028A-4	Sequence 4, Appli
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c 15	1632.8	30.9	5285	21	US-10-950-050-10	Sequence 10, Appl
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17	1603.8	30.4	3534	14	US-10-021-403A-10	Sequence 10, Appl
18	1603.8	30.4	3534	14	US-10-021-403A-9	Sequence 9, Appli
19	1603.8	30.4	3534	17	US-10-395-709-11	Sequence 11, Appl
20	1603.8	30.4	3534	17	US-10-395-709-12	Sequence 12, Appl
21	1603.8	30.4	3534	17	US-10-395-709-13	Sequence 13, Appl
22	1603.8	30.4	3534	17	US-10-395-709-14	Sequence 14, Appl
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ALIGNMENTS

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; Sequence 36, Application US/09921143
; Publication No. US2003021592lA1
; GENERAL INFORMATION:
; APPLICANT: Coleman, Timothy
; TITLE OF INVENTION: Vascular Endothelial Growth Factor-2
; FILE REFERENCE: PF112P6
; CURRENT APPLICATION NUMBER: US/09/921,143
; CURRENT FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 60/223,276
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 36
; LENGTH: 5283
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-921-143-36

Query Match   100.0%; Score 5283; DB 10; Length 5283;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5283; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

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Qy   61 TACCATGGTGATGCGGTTTGGCAGTACATCAATGGCGTGGATAGCGGTTTGACTCACG 120
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Qy 3421 AACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGCAGCAGCCACT 3480
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Db 3421 AACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGCAGCAGCCACT 3480

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Qy 3541 CCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGGCTCTGTCGTGAAGCCAGTT 3600
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Db 3541 CCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGGCTCTGTCGTGAAGCCAGTT 3600

Qy 3601 ACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCCGGT 3660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3601 ACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCCGGT 3660

Qy 3661 GGTTTTTTGTTGCAAGCAGCAGATTACGCGCAGAATAAAAGGATCTCAAGAAGATCCT 3720
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Db 3661 GGTTTTTTGTTGCAAGCAGCAGATTACGCGCAGAATAAAAGGATCTCAAGAAGATCCT 3720

Qy 3721 TTGATCTTTTCTACGGGGTCTGACGCTCAGTGGAACGAAAACTCACGTTAAGGGATTTTG 3780
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Db 3721 TTGATCTTTTCTACGGGGTCTGACGCTCAGTGGAACGAAAACTCACGTTAAGGGATTTTG 3780

Qy 3781 GTCATGAGATTATCGTCGACCAAAGCGGCCATCGTGCCTCCCCACTCGTGTCCAGTTCGGGG 3840
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Db 3781 GTCATGAGATTATCGTCGACCAAAGCGGCCATCGTGCCTCCCCACTCGTGTCCAGTTCGGGG 3840

Qy 3841 GCATGATGGCCGAGGTCGTCCAGCCTCCAGCCAGCAGCAGTCGTGACAACCAACTCGGGGATCG 3900
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Db 3841 GCATGATGGCCGAGGTCGTCCAGCCTCCAGCCAGCAGCAGTCGTGACAACCAACTCGGGGATCG 3900

Qy 3901 TAGAACTCCGGGTGGGCGGAAGAACTCCAGGCATGAGATCCGGCTGGAGGGGATCG 3960
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Db 3901 TAGAACTCCGGGTGGGCGGAAGAACTCCAGGCATGAGATCCGGCTGGAGGGGATCG 3960

Qy 3961 AGCCCGGGGTGGGCGGAGGAAGAACTCCAGCATGAGATCCCGGCTGGAGGATCATCCAGCCG 4020
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Db 3961 AGCCCGGGGTGGGCGGAGGAAGAACTCCAGCATGAGATCCCGGCTGGAGGATCATCCAGCCG 4020

Qy 4021 GCGTCCCGGAAAACGATTCCAAGCCCAAACCTTTCATAGAAGGCGGGCGGTGAATCGAAA 4080
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Db 4021 GCGTCCCGGAAAACGATTCCAAGCCCAAACCTTTCATAGAAGGCGGGCGGTGAATCGAAA 4080

Qy 4081 TCTCGTGATGCGATATGTCCAGGTGGGCGTCGCTGGTCATTGAACCCCAGAGTCCCGCTC 4140
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Db 4081 TCTCGTGATGCGATATGTCCAGGTGGGCGTCGCTGGTCATTGAACCCCAGAGTCCCGCTC 4140

Qy 4141 AGAAGAACTCGTCAAGAACTCGTCAAGAGGCCTGCGAATCGGGAAGGCGGCATCGGAGGCGGGCGGCGGGATAC 4200
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Db 4141 AGAAGAACTCGTCAAGAACTCGTCAAGAGGCCTGCGAATCGGGAAGGCGGCATCGGAGGCGGGCGGCGGGATAC 4200

Qy 4201 CGTAAAGCACGAGGAGCGGTCAGCGCTCTTCAGCAATATCACGGG 4260
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Db 4201 CGTAAAGCACGAGGAGCGGTCAGCGCTCTTCAGCAATATCACGGG 4260

Qy 4261 TAGCCAACGCTATGTCCTGATAGCGGTCCGCGCCCACACCCAGCCAACGCCACAGTGATGAATC 4320
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Db 4261 TAGCCAACGCTATGTCCTGATAGCGGTCCGCGCCCACACCCAGCCAACGCCACAGTGATGAATC 4320

Qy 4321 CAGAAAAGCGGCCATTTTCCACCATGATATTCGGCAGCAGCAGGCCATGCCGGTCACGA 4380
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Db 4321 CAGAAAAGCGGCCATTTTCCACCATGATATTCGGCAGCAGCAGGCCATGCCGGTCACGA 4380

Qy 4381 CGAGATCCTCGCGTCGGGCGTCCTGCGTGGGAACAGTTCGGCTGGTAGGTCGTTCGC 4440
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Db 4381 CGAGATCCTCGCGTCGGGCGTCCTGCGTGGGAACAGTTCGGCTGGTAGGTCGTTCGC 4440

Qy 4441 GCCCCTGATGTCTTCGTCCGACAGTCATCCTCCAGATCATCGCTTCCAAGAACGCCGGCTTCATCCGGAGTAC 4500
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Qy 2281 TAAAGTGAGAGAAAGCTGGGCTAATCAGGGGGTCGCTCAGCTCCTCCTCCTAACTGGATTGT 2340
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Db 2281 TAAAGTGAGAGAAAGCTGGGCTAATCAGGGGGTCGCTCAGCTCCTCCTCCTAACTGGATTGT 2340

Qy 2341 CCTATGTGTCTTTGCTTCGTCTGCTGCTGCCCGTGTTGCTGACATGACCTCCCTG 2400
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Qy 2401 GCAGTGCACAACTGGAGCTGGGTGGAGGCCCGGGCAGGTGACCTTCAGACCTTGGCA 2460
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Qy 2461 CTGGGAGGTGGCCCGGCGAGAAGCGCGGCATCGTGGATCAGTGCTGCGCACCCAGCATCTGCTCT 2520
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Qy 2521 CTCTACCAACTGGAGAACTACTGCAACTAGGCCCACCACTACCCGTTCCACCCCTCTGCA 2580
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Qy 2641 TGGTGCGGGGAACATGAGTGGGGCTGGCTGGAGTGGTGGCCTAATCTATCGGCA 2700
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Qy 2701 GCTGTCTAGACGTAATCATGGTCATAGCTGTGTTCCGTGTGTGGTGTATCCGCTCACA 2760
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Db 2701 GCTGTCTAGACGTAATCATGGTCATAGCTGTGTTCCGTGTGTGGTGTATCCGCTCACA 2760

Qy 2761 ATTCCACACACAGAGCACATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGATAAGTG 2820
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Qy 2821 AGCTAACTCACATTAATTGCGTTGCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGG 2880
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Qy 2881 TGCCAGCTGCATTAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGC 2940
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Qy 2941 TCTTCCGCTTCCTCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTA 3000
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Db 2941 TCTTCCGCTTCCTCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTA 3000

Qy 3001 TCAGCTCACTCAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAG 3060
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Db 3001 TCAGCTCACTCAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAG 3060

Qy 3061 AACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCG 3120
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Db 3061 AACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCG 3120

Qy 3121 TTTTTCCATAGGCTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGG 3180
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Db 3121 TTTTTCCATAGGCTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGG 3180

Qy 3181 TGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTG 3240
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Db 3181 TCAGCTCACTCAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAG 3240

Qy 3241 CGTCTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGA 3300
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Db 3241 CGTCTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGA 3300

Qy 3301 AGCGGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGC 3360
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Db 3301 AGCGGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGC 3360

Qy 3361 TCCAAGCTGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGGTCGGCCTTATCCGGT 3420
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;   SOFTWARE: PatentIn version 3.1
;   SEQ ID NO 16
;   LENGTH: 8349
;   TYPE: DNA
;   ORGANISM: artificial sequence
;   FEATURE:
;   OTHER INFORMATION: completely synthesized
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(8349)
;   OTHER INFORMATION:
US-10-198-478-16

Query Match             42.4%;    Score 2240;   DB 16;   Length 8349;
Best Local Similarity   93.4%;    Pred. No. 0;
Matches 2409;  Conservative    0;  Mismatches  25;  Indels 144;  Gaps  1;

Qy    2706  CTAGACGTAATCATGTCATAGCTGTTCCTGTGTGAAATTGTTATCCGCTCACAATTCC  2765
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Db    5911  CTTGGCGTAATCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCC  5970

Qy    2766  ACACAACATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTA  2825
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Db    5971  ACACAACATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTA  6030

Qy    2826  ACTCACATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCA  2885
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Db    6031  ACTCACATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCA  6090

Qy    2886  GCTGCATTAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTGCGTATTGGGCGCTCTTC  2945
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    6091  GCTGCATTAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTGCGTATTGGGCGCTCTTC  6150

Qy    2946  CGCTTCCTCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCGGC  3005
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    6151  CGCTTCCTCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGC  6210

Qy    3006  TCACTCAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACAT  3065
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Db    6211  TCACTCAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACAT  6270

Qy    3066  GTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTT  3125
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    6271  GTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTT  6330

Qy    3126  CCATAGGCTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCG  3185
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Db    6331  CCATAGGCTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCG  6390

Qy    3186  AAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTC  3245
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Db    6391  AAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTC  6450

Qy    3246  TCCTGTTCCGACCCTGCCGCTTACCGGATACCGTCCGCCTTTCTCCCTTCGGGAAGCGT  3305
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    6451  TCCTGTTCCGACCCTGCCGCTTACCGGATACCGTCCGCCTTTCTCCCTTCGGGAAGCGT  6510

Qy    3306  GGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAA  3365
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    6511  GGCGCTTTCTCAATGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAA  6570

Qy    3366  GCTGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTA  3425
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Db    6571  GCTGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTA  6630

Qy    3426  TCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAA  3485
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Db    6631  TCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAA  6690

Qy    3486  CAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAA  3545
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Db    6691  CAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAA  6750
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Db    4441  GCCCCTGATGCTCTTCGTCCAGATCATCCTGATCGCACAAGACCGGCTTCCATCCGAGTAC  4500
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Qy    4501  GTGCTCGCTCGATGCGATGTTTCGCTTGGTGGTCGAATGGGCAGTAGGCCGGATCAAGCG  4560

Db    4501  GTGCTCGCTCGATGCGATGTTTCGCTTGGTGGTCGAATGGGCAGTAGGCCGGATCAAGCG  4560

Qy    4561  TATGCAGCCGCCGCATTGCATCAGCCATGATGACTTTCTCGGCAGGAGCAAGGTGAG  4620
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Db    4561  TATGCAGCCGCCGCATTGCATCAGCCATGATGACTTTCTCGGCAGGAGCAAGGTGAG  4620

Qy    4621  ATGACAGGAGATCCTGCCCCGGCACTTCGCCCAATAGCAGCCAGTCCCTTCCCGCTTCAG  4680
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Db    4621  ATGACAGGAGATCCTGCCCCGGCACTTCGCCCAATAGCAGCCAGTCCCTTCCCGCTTCAG  4680

Qy    4681  TGACAACGTCGAGCAACAGTCGCGCAAGGAACGCCCGTCGTGGCCAGCCACGATAGCCGCG  4740
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4681  TGACAACGTCGAGCAACAGTCGCGCAAGGAACGCCCGTCGTGGCCAGCCACGATAGCCGCG  4740

Qy    4741  CTGCCTCGTCCGTCGATCATTCAGGGCACCGGACAGGTCGGTCTTGACAAAAAGAACCG  4800
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4741  CTGCCTCGTCCGTCGATCATTCAGGGCACCGGACAGGTCGGTCTTGACAAAAAGAACCG  4800

Qy    4801  GGGCGCCCTGCGCTGACAGCCGGAACACGGCGGCATCAGAGCAGCCGATTGTCTGTTGTG  4860
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4801  GGGCGCCCTGCGCTGACAGCCGGAACACGGCGGCATCAGAGCAGCCGATTGTCTGTTGTG  4860

Qy    4861  CCCAGTCATAGCCGAATAGCCTCTCCACCCAAGCGGCCGGAGAACCTGCGTGCAATCCAT  4920
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4861  CCCAGTCATAGCCGAATAGCCTCTCCACCCAAGCGGCCGGAGAACCTGCGTGCAATCCAT  4920

Qy    4921  CTTGTTCAATCATGCGGAAACGATCCTCATCCTGTCTCTTGATCGATATCTTGATCCCCTGC  4980
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4921  CTTGTTCAATCATGCGGAAACGATCCTCATCCTGTCTCTTGATCAGATCTTGATCCCCTGC  4980

Qy    4981  GCCATCAGATCCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTGCAGGGCTTCCCAACCT  5040
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Db    4981  GCCATCAGATCCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTGCAGGGCTTCCCAACCT  5040

Qy    5041  TACCAGAGGGCGCCCCAGCTGGCAATTCCGGTTCGCTTGCTGTCCATAAAACCGCCAGT  5100
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Db    5041  TACCAGAGGGCGCCCCAGCTGGCAATTCCGGTTCGCTTGCTGTCCATAAAACCGCCCAGT  5100

Qy    5101  CTAGCTATCGGCATGCATGTAAGCCCACTGCAAGCTACCTGCTTTCTCTTTGCGCTTGCGTTT  5160
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Db    5101  CTAGCTATCGGCATGCATGTTAAGCCCACTGCAAGCTACCTGCTTTCTCTTTGCGCTTGCGTTT  5160

Qy    5161  CCCTTGTCCAGATAGCCCAGTAGCTGACATTCATCCGGGGTCAGCACCGTTTCTGCGGAC  5220
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Db    5161  CCCTTGTCCAGATAGCCCAGTAGCTGACATTCATCCGGGGTCAGCACCGTTTCTGCGGAC  5220

Qy    5221  TGGCTTTCTACGTGTTCCGCTTCCTTTAGCAGCCCTTGCGCCCTGAGTGCTTGCGGCAGC  5280
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Db    5221  TGGCTTTCTACGTGTTCCGCTTCCTTTAGCAGCCCTTGCGCCCTGAGTGCTTGCGGCAGC  5280

Qy    5281  GTG  5283
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Db    5281  GTG  5283
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RESULT 2
US-10-198-478-16
;  Sequence 16, Application US/10198478
;  Publication No. US20030188336A1
;  GENERAL INFORMATION:
;  APPLICANT: Corbin, David R.
;  APPLICANT: Romano, Charles P.
;  TITLE OF INVENTION: Improved Methods for Transforming Plants to Express delta-Endotoxin
;  FILE REFERENCE: 38-21 (13547) B
;  CURRENT APPLICATION NUMBER: US/10/198,478
;  CURRENT FILING DATE: 2002-11-12
;  PRIOR APPLICATION NUMBER: 09/186, 002
;  PRIOR FILING DATE: 1998-11-04
;  NUMBER OF SEQ ID NOS: 18
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Qy   3546 CTACGGCTACACTAGAGAACAGTATTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTT 3605
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Db   6751 CTACGGCTACACTAGAGAGGACACAGTATTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTT 6810

Qy   3606 CCGAAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAACCACCGCTGTAGCGGTGGTT 3665
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Qy   3666 TTTTGTTTGTCAAGCAGCAGATTACGCGCAGAAAAAGGATCTCAAGAAGATCCTTTGAT 3725
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Db   6871 TTTTGTTTGTCAAGCAGCAGATTACGCGCAGAAAAAGGATCTCAAGAAGATCCTTTGAT 6930

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Qy   3786 GAGATTATCGTCGACCAAAGCGGCCATCGTGCCTCCCACTCCTGCAGTTCGGGGCATG 3845
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Db   6991 GAGATTATCAAAAAGATCTTCACCTAGATCCTT-------------------------- 7024

Qy   3846 GATGCGCGGGATAGCCGCGTGGTTTCCTGATGCCGACGGATTTGCACTGGTCCGGGTAGAA 3905
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Db   7025 -------------------------------------------------------- 7024

Qy   3906 CTCCGCGAGTCGTCCAGCCTCAGGCAGCAGTCGAACCAACTCGCCGAGGGGATCGAGCCCC 3965
Db   7025 --------------------------------------------------------TT 7026

Qy   3966 GGGGGTGGGCGGAGAACTCCAGCATGAGATCCCCGCCGCTGGAGGATCATCCAGCCGCGTC 4025
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Qy   4026 CCGGAAAAACGATTCCGAAGCCCAACCTTTCATAGAAGGCGGTGGAATCGAAATTCTCG 4085
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Db   7207 AACTCGTCAAGAAGGCGATAGAAGGCGATGCGCTGCGAATCGGCGGCGGCGGATACCGTAA 7266

Qy   4206 AGCACGAGGAAGCGGTCAGCCCATTCGCCGCCAAGCTCTTCAGCAATATCACGGGTAGCC 4265
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Db   7267 AGCACGAGGAAGCGGTCAGCCCATTCGCCGCCAAGCTCTTCAGCAATATCACGGGTAGCC 7326

Qy   4266 AACGCTATGTCCTGATAGCGGTCCGCCACACCCAGCCGGCCACAGTCGATGAATCCAGA 4325
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Db   7327 AACGCTATGTCCTGATAGCGGTCCGCCACACCCAGCCGGCCACAGTCGATGAATCCAGA 7386

Qy   4326 AAGCCGGCCATTTTCCACCATGATATTCGGCAAGCAGGCATCGCCATGGGTCACGACGAGA 4385
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7387 AAGCCGGCCATTTTCCACCATGATATTCGGCAAGCAGGCATCGCCATGGGTCACGACGAGA 7446

Qy   4386 TCCTCGCCGTCGGGCATGCGCGCCTTGAGCCTGGCGAACAGTTCGGCTGGCGCGAGCCCC 4445
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7447 TCCTCGCCGTCGGGCATGCGCGCCTTGAGCCTGGCGAACAGTTCGGCTGGCGCGAGCCCC 7506

Qy   4446 TGATGCTCTTCGTCCAGATCATCCTGATCGACAAGACCGGCTTCCATCCGAGTACGTGCT 4505
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7507 TGATGCTCTTCGTCCAGATCATCCTGATCGACAAGACCGGCTTCCATCCGAGTACGTGCT 7566

Qy   4506 CGCTCGATGCGATGTTTCGCTTGGTGGTCGAATGGGCAGGTAGCCGGATCAAGCGTATGC 4565
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7567 CGCTCGATGCGATGTTTCGCTTGGTGGTCGAATGGGCAGGTAGCCGGATCAAGCGTATGC 7626

Qy   4566 AGCCGCCGCATTCGATCAGCCATGATGGATATTTCTCGGCAGGAGCAAGGTGAGATGAC 4625
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Db   7627 AGCCGCCGCATTCGATCAGCCATGATGGATACTTTCTCGGCAGGAGCAAGGTGAGATGAC 7686

Qy   4626 AGGAGATCCTGCCCCGGCACTTCGCCCAATAGCAGCCAGTCCCTTCCCGCTTCAGTGACA 4685
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Db   7687 AGGAGATCCTGCCCCGGCACTTCGCCCAATAGCAGCCAGTCCCTTCCCGCTTCAGTGACA 7746

Qy   4686 ACGTCGAGCACAGCTGCGCAAGGAACGCCCGTCGTGGCCAGCCACGATAGCCGCGCTGCC 4745
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7747 ACGTCGAGCACAGCTGCGCAAGGAACGCCCGTCGTGGCCAGCCACGATAGCCGCGCTGCC 7806

Qy   4746 TCGTCCTGCAGTTCATTCAGGGCACCGGACAGGTCGGTCTTGACAAAAAGAACCGGGGGC 4805
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7807 TCGTCCTGCAGTTCATTCAGGGCACCGGACAGGTCGGTCTTGACAAAAAGAACCGGGGGC 7866

Qy   4806 CCCTGCGCTGACAGCCGGAACACGGCGGCATCAGAGCAGCCGATTGTCTGTTGTGCCCAG 4865
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7867 CCCTGCGCTGACAGCCGGAACACGGCGGCATCAGAGCAGCCGATTGTCTGTTGTGCCCAG 7926

Qy   4866 TCATAGCCGAATAGCCTCTCCACCCAAGCGGCCGGAGAACCTGCGTGCAATCATCTTGT 4925
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7927 TCATAGCCGAATAGCCTCTCCACCCAAGCGGCCGGAGAACCTGCGTGCAATCCATCTTGT 7986

Qy   4926 TCAATCATGCGAAACGATCCTCGTCTCCTGATCAGATCTTGATCCCCTGCGCCAT 4985
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7987 TCAATCATGCGAAACGATCCTCGTCTCCTGATCAGATCTTGATCCCCTGCGCGCCAT 8046

Qy   4986 CAGATCCTTCGGCGCGATTCCGGTTCGCTTGCTGTCGTCGTCATCCAGTTTACTTTGCAGG 5045
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   8047 CAGATCCTTGGCGCGATTCCGGTTCGCTTGCTGTCGTCGTCATCCAGTTTACTTTGCAGG 8106

Qy   5046 GAGGGGCGCCCCAGCTGGCAATTCCGGTTCGCTTGCTGTCCATAAAACCGCCCAGTCTAGC 5105
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   8107 GAGGGGCGCCCCAGCTGGCAATTCCGGTTCGCTTGCTGTCCATAAAACCGCCCAGTCTAGC 8166

Qy   5106 TATCGCCATGTAAGCCCACTGCAAGCTACCTGCTTTCTCTTTGCGCTTGCGTTTTCCCTT 5165
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   8167 TATCGCCATGTAAGCCCACTGCAAGCTACCTGCTTTCTCTTTGCGCTTGCGTTTTCCCTT 8226

Qy   5166 GTCCAGATAGCCCAGTAGCTGACATTCATCCGGGGTCAGCACCGTTTCTGCGGACTGCT 5225
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   8227 GTCCAGATAGCCCAGTAGCTGACATTCATCCGGGGTCAGCACCGTTTCTGCGGACTGGCT 8286

Qy   5226 TTCTACGTGTTCCGCTTCCTTTAGCAGCCCTTCCGCCCTGAGTGCTTGCGGCAGCGTG 5283
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   8287 TTCTACGTGTTCCGCTTCCTTTAGCAGCCCTTCCGCCCTGAGTGCTTGCGGCAGCGTG 8344
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Query Match    42.4%;   Score 2240;   DB 20;   Length 11546;
Best Local Similarity  93.4%;   Pred. No. 0;
Matches 2409;   Conservative   0;   Mismatches   25;   Indels 144;   Gaps  1;

Qy   2706 CTAGACGTAATCATGTCATAGCTGTTCCGTGTGTGAAATTGTTATCCGCTCACAATTCC 2765
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Db  10188 GAGATTATCAAAAGGATCTTCACCTAGATCCTT----------------------------  10221
           ||||||
Qy   3846 GATGCCGGATAGCCGTGCTGGTTCCTGGATGCCGACGATTTGCACTGCCGGTAGAA         3905

Db  10222 ------------------------------------------------------------  10221
           ||||||
Qy   3906 CTCCGCGAGGTCGTCCAGCCTCAGGCAGCAGCTGAACCAACTCGCGAGGGGATCGAGCCC   3965

Db  10222 --------------------------------------------------------TT   10223
           ||||||
Qy   3966 GGGGTTGGCGAAGAACTCCAGCATGAGAATCCCCGCGTCGAGAGATCATCCAGCGCGTC    4025

Db  10224 GGGGTTGGCGAAGAACTCCAGCATGAGAATCCCCGCGTCGAGAGATCATCCAGCGCGTC   10283
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   2886 GCTGCATTAATGAATCGGCCAACGCGGGGGAGAGGCGGTTGCGTATTGGGCGCTCTTC    2945

Db   9288 GCTGCATTAATGAATCGGCCAACGCGGGGGAGAGGCGGTTGCGTATTGGGCGCTCTTC    9347
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Qy  10284 CCGGAAAAACGATTCCGAAGCCAACCTTTCATAGAAGGCGCGGTGGAATCGAAATCTCG   10343

Db   2946 CGCTTCCTCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGC   3005
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   9408 CGCTTCCTCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGC   9467

Db  10344 TGATGCAGGTTGGGCGTCGCTTGGTCGGTCATTTCGAACCCCAGAGTCCCGCTCAGAAG   10403
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   3066 GTGAGCAAAAGGCCAGGAACCGTAAAAAAGGCCGCGTTGCTGGCGTTTT             3125

Db   9468 GTGAGCAAAAGGCCAGGAACCGTAAAAAAGGCCGCGTTGCTGGCGTTTT             9527
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  10404 AACTCGTCAAGAAGGCCGATAGAAGGCGATGCGCTGCGAATCGGGAGCGGCGGATACCGTAA  10463

Db   3126 CCATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCG   3185
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  10464 AGCACGAGGAAGCGGTCAGCCATTCGCCGCCAAGCTCTTCAGCAATATCACGGCTAGCC   10523

Db   9528 CCATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCG   9587
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4266 AACGCTATGTCCTGATAGCCGGTCCCGGTTCCCCTGGAAGCTCCCTCGTGCGCTC        4325

Db   3186 AAACCCGACGAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTC   3245
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  10524 AACGCTATGTCCTGATAGCCGGTCCCGGTTCCCCTGGAAGCTCCCTCGTGCGCTC       10583

Db   9588 AAACCCGACGAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTC  9647
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4326 AAGCCGGCCATTTCCACCATGATATTCGGCAAGCAGGCGATCGCCATGGGTCACGACGAGA  4385

Db   3246 TCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGT   3305
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Qy  10584 AAGCCGGCCATTTCCACCATGATATTCGGCAAGCAGGCGATCGCCATGGGTCACGACGAGA 10643

Db   9648 TCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGT  9707
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4386 TCCTCGCGTCGGGCATGCGCGCCTTGAGCGTGGCGGAACAGTTCGGCTGCGGCGGAGCCCC  4445

Db   3306 GGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAA   3365
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  10644 TCCTCGCGTCGGGCATGCGCGCCTTGAGCGTGGCGGAACAGTTCGGCTGCGGCGGAGCCCC 10703

Db   9708 GGGCGCTTTCTCAATGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAA  9767
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4446 TGATGCTCTTCGTCCAGATCATCCTGATCGACAAGACCGGCTTCATCCGAGTACGTGCT    4505

Db   3366 GCTGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTA   3425
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Qy  10704 TGATGCTCTTCGTCCAGATCATCCTGATCGACAAGACCGGCTTCATCCGAGTACGTGCT   10763

Db   9768 GCTGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTA  9827
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Qy   4506 CGCTCGATGCGATGTTTCGCTTGGTGGTCGAATGGGCAGGTAGCCGGATCAAGCGTATGC  4565

Db   3426 TCGTCTTGAGTCCAACCCGGTAAGACACTTATCCGCAGCAGCCACTGGCAGCAGCCA     3485
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Qy  10764 CGCTCGATGCGATGTTTCGCTTGGTGGTCGAATGGGCAGGTAGCCGGATCAAGCGTATGC 10823

Db   9828 TCGTCTTGAGTCCAACCCGGTAAGACACTTATCCGCAGCAGCCACTGGCAGCAGCCA    9887
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Qy   4566 AGCCCGCCGCCATTCGATCAGCCATGATACTTTTCTCGGCAGGAGCCAGGTGAGATGAC   4625

Db   3486 CAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAA   3545
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Qy  10824 AGCCCGCCGCCATTCGATCAGCCATGATACTTTTCTCGGCAGGAGCCAGGTGAGATGAC   10883

Db   9888 CAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAA  9947
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4626 AGGAGATCCTGCCCCGGCACTCGCCCAATAGCAGCCAGTCCTTCCGCAGTTACCTT      4685

Db   3546 CTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCACTCTGCGCTCTGAAGCCAGTTACCTT   3605
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Qy  10944 AGGAGATCCTGCCCCGGCACTCGCCCAATAGCAGCCAGTCCTTCCGCAGTTACCTT     11003

Db  10884 AGGAGATCCTGCCCCGGCACTCGCCCAATAGCAGCCAGTCCTTCCGCAGTTACCTT     10943
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Qy   4686 ACGTCGAGCACAGCTGTGCGCAAGGAACGCCCGTGTGGCCAGCCACTGGCGCTGCC    4745

Db   3606 CGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTT   3665
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Qy  10008 CGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTT  10067

Db   4746 TCGTCCTGCAGTTCATTCAGGGCACCGGACAGGTCGGTCTTGACAAAAAGAACCGGCGC   4805
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  11004 TCGTCCTGCGAGTTCATTCAGGGCACCGGACAGGTCGGTCTTGACAAAAAGAACCGGCGC  11063

Db   3666 TTTTGTTTGCAAGCAGCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGAT   3725
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  10068 TTTTTGTTTGCAAGCAGCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGAT  10127

Db   4806 CCCTGGCTGACGAGCGTCAGTGGAACGAAACTCACGTTAAGGGATTTTGGTCAT        4865
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Qy  11064 CCCTGGCTGACGAGCGTCAGTGGAACGAAACTCACGTTAAGGGATTTTGGTCAT       11123

Db   3726 CTTTTCTACGGGGTCTGACGGCTCAGCGGAACGAAACTCACGTTAAGGGATTTTGGTCAT   3785
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  10128 CTTTTTCTACGGGGTCTGACGGCTCAGCGGAACGAAACTCACGTTAAGGGATTTTGGTCAT 10187

Db   4866 TCATAGCCGAATAGCCTCTCCACCCAAGCGGCCGGAGAACCTGCGTGCAATCCATCTTGT   4925
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   3786 GAGATTATCGTCGACCAAAGCGGCCATCGTGCCTCCCCACTCGTGCGGCCGTCGGGGATG    3845

Db  11124 TCATAGCCGAATAGCCTCTCCACCCAAGCGGCCGGAGAACCTGCGTGCAATCCATCTTGT   11183
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Qy  3427 CGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAAC 3486
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Db  4500 CGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAAC 4441

Qy  3487 AGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAAC 3546
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Db  4440 AGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAAC 4381

Qy  3547 TACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGGTCCTCGTGCGAGCCAGTTACCTTC 3606
         ||||||||||||||||||| |||||||||| ||||| || ||||||| ||||| ||||| |
Db  4380 TACGGCTACACTAGAAGGACAGTATTTGGTATCTGCCGCTCGTGCTGCTCGTGCGAGCCAGTTACCTTC 4321

Qy  3607 GGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAACCACCGCTGGTAGCGGTGGTTTTT 3666
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4320 GGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAACCACCGCTGGTAGCGGTGGTTTTT 4261

Qy  3667 TTTGTTTGCAAGCAGCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGATC 3726
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Db  4260 TTTGTTTGCAAGCAGCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGATC 4201

Qy  3727 TTTTCTACGGGGTCTGACGCTCAGTGGAACGAAAACTCACGTTAAGGGATTTTGGTCATG 3786
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db  4200 TTTTCTACGGGGTCTGACGCTCAGTGGAACGAAAACTCACGTTAAGGGATTTTGGTCAT- 4142

Qy  3787 AGATTATCGTCCACCAAAGCGGCCATCGTCCCCACTCGTGCCTCCCACTCCTGCAGTGG 3846
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Db  4141 ------------------------------------------------------------ 4142

Qy  3847 ATGCGCGGATAGCCGCTGCTGTTTCTGATGCCGACGGATTTGCACTGCCGGTAGAAC 3906
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Db  4141 ------------------------------------------------------------ 4142

Qy  3907 TCCGCGAGGTCGTCCACCCTCAGGCAGCAGCTGAACCAACTCGCGAGGGGATCGAGCCG 3966
                                                                ||||||
Db  4141 -------------------------------------------------------GCCCG 4137

Qy  3967 GGGTGGCGGAAGAACTCCAGCATGAGATCCCCGCGCTGGAGGATCATCCAGCCGGCCGTCC 4026
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4136 GGGTGGCGGAAGAACTCCAGCATGAGATCCCCGCGCTGGAGGATCATCCAGCCGGCCGTCC 4077

Qy  4027 CGGAAAACGATTCCGAAGCCCAACCTTTCATAGAAGGCGGCGGTGGAATCGAAATCTCGT 4086
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Db  4076 CGGAAAACGATTCCGAAGCCCAACCTTTCATAGAAGGCGGCGGTGGAATCGAAATCTCGT 4017

Qy  4087 GATGGCAGGTTGGGCGTCGCGGTGGTCGTGCATTTGAACCCGGATCGGAATCGGGAATCG 4146
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4016 GATGGCAGGTTGGGCGTCGCGGTGGTCGTGCATTTGAACCCGGATCGGAATCGGGAATCG 3957

Qy  4147 ACTCGTCAAGAAGGCGATAGAAGGCGATGCGCTGCGAATCGGGAGAGGCGGCGGATACCGGTAAA 4206
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Db  3956 ACTCGTCAAGAAGGCGATAGAAGGCGATGCGCTGCGAATCGGGAGAGGCGGCGGATACCGGTAAA 3897

Qy  4207 GCACGAGGAAGCGGTCAGCCCATTCGCGCGCCAAGCTCTTCAGCAATATCACGGGTAGCCA 4266
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Db  3896 GCACGAGGAAGCGGTCAGCCCATTCGCGCGCCAAGCTCTTCAGCAATATCACGGGTAGCCA 3837

Qy  4267 ACGCTATGTCCTGATAGCGGTCCTGATAGCGGTCCCAGCAGTCGATGAATCGATCAGAAA 4326
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3836 ACGCTATGTCCTGATAGCGGTCCTGATAGCGGTCCCAGCAGTCGATGAATCGATCAGAAA 3777

Qy  4327 AGCGGCCATTTCCACCATGATATTCGGCAAGCAGGCATCGCCATGGTCACGACGAGAT 4386
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3776 AGCGGCCATTTCCACCATGATATTCGGCAAGCAGGCATCGCCATGGTCACGACGAGAT 3717

Qy  4387 CCTCGCCGTCGGGCATGCGCGCCTTGAGCCTGGTCGTTCGGCTCGCTCCAAG 4446
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Db  3716 CCTCGCCGTCGGGCATGCGCGCCTTGAGCCTGGTCGTTCGGCTCGCTCCAAG 3657

Qy  4447 GATGCTCTTCGTCGCAGATCATCCTGATCGACAAGACCGGCTTCATCCGAGTACGTGCTC 4506
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Db  3656 GATGCTCTTCGTCGCAGATCATCCTGATCGACAAGACCGGCTTCATCCGAGTACGTGCTC 3597

Qy  4507 GCTCGATGCGATGTTTCGCTTGGTGTGTCGGATGGGCAGGTAGCCGATCAAGCGTATGCA 4566
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RESULT 4
US-10-322-360-1/c
; Sequence 1, Application US/10322360
; Publication No. US2003016594GA1
; GENERAL INFORMATION:
;   APPLICANT: Evans, Glen A.
;   TITLE OF INVENTION: A Method for the Complete Chemical
;   TITLE OF INVENTION:  Synthesis and Assembly of Genes and Genomes
;   FILE REFERENCE: P-EA 5511
;   CURRENT APPLICATION NUMBER: US/10/322,360
;   CURRENT FILING DATE: 2002-12-17
;   PRIOR APPLICATION NUMBER: US 09/554,929
;   PRIOR FILING DATE: 2000-05-12
;   NUMBER OF SEQ ID NOS: 193
;   SOFTWARE: PatentIn for Windows Version 4.0
;   SEQ ID NO 1
;   LENGTH: 4800
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic plasmid
US-10-322-360-1

Query Match  33.9%;  Score 1793.4;  DB 16;  Length 4800;
Best Local Similarity  91.8%;  Pred. No. 0;
Matches 1980;  Conservative  0;  Mismatches  1;  Indels  176;  Gaps  1;

Qy  3127 CATAGGCTCCGCCCCCCTGACGAGCAGCATCACAAAAATCGACGGCTCAAGTCAGAGGTGGGCGA 3186
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Db  4800 CATAGGCTCCGCCCCCCTGACGAGCAGCATCACAAAAATCGACGGCTCAAGTCAGAGGTGGGCGA 4741

Qy  3187 AACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCT 3246
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Db  4740 AACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCT 4681

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Qy  3307 GCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAG 3366
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Db  4620 GCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAG 4561

Qy  3367 CTGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTAT 3426
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Db  4560 CTGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTAT 4501
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Db   3596 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
          GCTCGATGCGATGTTTCGCTTGGTGGTCGAATGGGCAGTAGCCGGATCAAGCGTATGCA 3537

Qy   4567 GCCGCGCAATTGCATCAGCCATGATGATACTTTCTGGCAGGAGCAAGTGAGATGACA 4626
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Db   3536 GCCGCGCAATTGCATCAGCCATGATGGATACTTTCTGGCAGGAGCAAGTGAGATGACA 3477

Qy   4627 GGAGATCCTGCTGCCCCGGCACTTCGCCCAATAGCAGCCAGTCCCTTCCCGCTTCAGTGACAA 4686
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Db   3476 GGAGATCCTGCCCCCGGCACTTCGCCCAATAGCAGCCAGTCCCTTCCCGCTTCAGTGACAA 3417

Qy   4687 CGTCCAGCACAGCAGCTGCGCAAGGAACGCCCGTGGCCAGCACGATAGCCGCGCTGCCT 4746
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Db   3416 CGTCCAGCACAGCAGCTGCGCAAGGAACGCCCGTGGCCAGCACGATAGCCGCGCTGCCT 3357

Qy   4747 CGTCCTGCAGTTCATTCAGGGCACCGGACAGAGGTCGGTCTTGACAAAAGAACCGGCGCC 4806
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Db   3356 CGTCCTGCAGTTCATTCAGGGCACCGGACAGAGGTCGGTCTTGACAAAAGAACCGGCGCC 3297

Qy   4807 CCTGGCTGACAGCAGCGGAACACGGCGGCATCAGAGCAGCCGATTGTCTTGTGTGCCCAGT 4866
          |||||||||||||||||||||||||||||||||||||||||||||| |||||||||||||
Db   3296 CCTGGCTGACAGCAGCGGAACACGGCGGCATCAGAGCAGCCGATTGTCTGTGTGCCCAGT 3237

Qy   4867 CATAGCCGAATAGCCTCTCCACCCAAGCGGCCGGAGAACCTGCGTGCAATCCATCCTTGTT 4926
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3236 CATAGCCGAATAGCCTCTCCACCCAAGCGGCCGGAGAACCTGCGTGCAATCCATCCTTGTT 3177

Qy   4927 CAATCATGCGAAACGATCCTCATCCTGTCTTGATCAGATCTTGATCCCCTGCGCCATC 4986
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3176 CAATCATGCGAAACGATCCTCATCCTGTCTTGATCAGATCTTGATCCCCTGCGCCATC 3117

Qy   4987 AGATCCTTGCGCGGCAAGAAAGCCATCCAGTTTACTTGCAGGGCGTTCCAAACCTTACCAG 5046
          ||||||||| |||||||||||||||||||||||||||||||||||| |||||||||||||
Db   3116 AGATCCTTGGGCGGCAAGAAAGCCATCCAGTTTACTTGCAGGGCGTTCCCAAACCTTACCAG 3057

Qy   5047 AGGGGCCCCAGCTGGCAATTCCGGTTCGCTTGCTGTCCATAAAACCGGCCAGTCTAGCT 5106
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3056 AGGGGCCCCAGCTGGCAATTCCGGTTCGCTTGCTGTCCATAAAACCGGCCAGTCTAGCT 2997

Qy   5107 ATCGGCATGTGAAGCCACTGCAAGCTACCTGCTTTCTCTTTGCGTTTGCGTTTCCCTTG 5166
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2996 ATCGGCATGTGAAGCCACTGCAAGCTACCTGCTTTCTCTTTGCGTTTGCGTTTCCCTTG 2937

Qy   5167 TCCAGATAGCCCAGTAGCTGACATTCATCCGGGGTCAGCCAGCCGTTTCTGCGGACTGGCTT 5226
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2936 TCCAGATAGCCCAGTAGCTGACATTCATCCGGGGTCAGCCAGCCGTTTCTGCGGACTGGCTT 2877

Qy   5227 TCTACGTGTTCCGCTTCCTTTAGCAGCCCGTTGCGCTTGCTGCTGAGTGTCGCGGCAGCGGTG 5283
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2876 TCTACGTGTTCCGCTTCCTTTAGCAGCCCGTTGCGCTTGCTGCTGAGTGTCGCGGCAGCGGTG 2820
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Qy   2706 CTAGACGTAATCATCGTCATAGCTGTTCCTGTGTGAAATTGTTATCCGCTCACAATTCC 2765
          |||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1977 CTTGGCGTAATCATCGTCATAGCTGTTCCTGTGTGAAATTGTTATCCGCTCACAATTCC 2036

Qy   2766 ACACACATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTA 2825
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2037 ACACACATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTA 2096

Qy   2826 ACTCACATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCA 2885
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2097 ACTCACATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCA 2156

Qy   2886 GCTGCATTAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTC 2945
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2157 GCTGCATTAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTC 2216

Qy   2946 CGCTTCCTCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGC 3005
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2217 CGCTTCCTCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGC 2276

Qy   3006 TCACTCAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACAT 3065
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2277 TCACTCAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACAT 2336

Qy   3066 GTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTT 3125
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2337 GTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTT 2396

Qy   3126 CCATAGGCTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCG 3185
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2397 CCATAGGCTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCG 2456

Qy   3186 AAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTC 3245
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2457 AAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTC 2516

Qy   3246 TCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGT 3305
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Db   2517 TCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGT 2576

Qy   3306 GGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAA 3365
          ||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db   2577 GGCGCTTTCTCAATGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAA 2636

Qy   3366 GCTGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTA 3425
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2637 GCTGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTA 2696

Qy   3426 TCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAA 3485
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2697 TCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAA 2756

Qy   3486 CAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAA 3545
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Db   2757 CAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAA 2816

Qy   3546 CTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTT 3605
          ||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db   2817 CTACGGCTACACTAGAAGGACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTT 2876

Qy   3606 CGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTT 3665
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Db   2877 CGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTT 2936

Qy   3666 TTTTGTTTGCAAGCAGCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGAT 3725
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RESULT 6
US-10-811-028A-6
; Sequence 6, Application US/10811028A
; Publication No. US20050043258A1
; GENERAL INFORMATION:
; APPLICANT: Bennett, Michael
; APPLICANT: Chen, Yen-Ju
; APPLICANT: Genteric, Inc.
; TITLE OF INVENTION: Methods of Treating Xerostomia and Xerophthalmia
; FILE REFERENCE: 020714-00241US
; CURRENT APPLICATION NUMBER: US/10/811,028A
; CURRENT FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: US 60/458,793
; PRIOR FILING DATE: 2003-03-26
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 4187
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:pMB1-EcSOD
; OTHER INFORMATION: plasmid expression vector
US-10-811-028A-6

Query Match   32.1%; Score 1697.8; DB 21; Length 4187;
Best Local Similarity   86.7%; Pred. No. 0;
Matches 1980; Conservative   0; Mismatches 102; Indels 201; Gaps   2;

Db 3345 AACTCGTCAAGAAGGCGATAGAAGGCGATGGCTGCGAATCGGGAGCGGCGGCGGGATACCGTAA 3404
Qy 4206 AGCACGAGGAAGGCGGTCAGCCCATTGCGCGCCAAGCTCTTCAGCAATATCACGGGTAGCC 4265
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3405 AGCACGAGGAAGGCGGTCAGCCCATTGCGCGCCAAGCTCTTCAGCAATATCACGGGTAGCC 3464

Qy 4266 AACGCTATGTCCTGATAGCGGTCCGGCAACACCCAGCCGACCAGTCGATGAATCCAGAA 4325
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Db 3465 AACGCTATGTCCTGATAGCGGTCCGGCAACACCCAGCCGACCAGTCGATGAATCCAGAA 3524

Qy 4326 AAGCGGCCATTTCCACCATGATATTCGGCAACAGCAGCATCGCCATGGGTCACGACGAGA 4385
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3525 AAGCGGCCATTTCCACCATGATATTCGGCAACAGCAGCATCGCCATGGGTCACGACGAGA 3584

Qy 4386 TCCTCCGCGTCGGGCATGCGCGCCTTGAGCCTGGCGGAACAGTTCGGCTGGCGCGAGCCCC 4445
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3585 TCCTCCGCGTCGGGCATGCGCGCCTTGAGCCTGGCGGAACAGTTCGGCTGGCGCGAGCCCC 3644

Qy 4446 TGATGCTCTTCGTCCAGATCATCCTGATCGACAAGACACCGGCTTCCATCCGAGTACGTGCT 4505
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3645 TGATGCTCTTCGTCCAGATCATCCTGATCGACAAGACACCGGCTTCCATCCGAGTACGTGCT 3704

Qy 4506 CGCTCGATGCGATGTTTCGCTTGGTGTGGTGAATGGGCAGGAGCAGCGGCAGAGCGTATGC 4565
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3705 CGCTCGATGCGATGTTTCGCTTGGTGTGGTGAATGGGCAGGAGCAGCGGCAGAGCGTATGC 3764

Qy 4566 AGCCGCGCCATTGCATCAGCCCATGATGGAATACTTTCTCGGCAGGAGCGCGTGAGATGAC 4625
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Db 3765 AGCCGCGCCATTGCATCAGCCCATGATGGAATACTTTCTCGGCAGGAGCGCGTGAGATGAC 3824

Qy 4626 AGGAGATTCCTGCCCCGCACTTCGCCCAATAGCAGCGACTTCGGCCAGTCCCTTCCGCTTCAGTGACA 4685
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Db 3825 AGGAGATTCCTGCCCCGCACTTCGCCCAATAGCAGCGACTTCGGCCAGTCCCTTCCGCTTCAGTGACA 3884

Qy 4686 ACGTCGAGCACAGCTGCGCAAGGAACCCCGTGCGGCCAGCCACGATAGCCGCGCTGCC 4745
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Db 3885 ACGTCGAGCACAGCTGCGCAAGGAACCCCGTGCGGCCAGCCACGATAGCCGCGCTGCC 3944

Qy 4746 TCGTCCTGCAGTTCATTCAGGGCACCGGACAGGTCCGTCTTGACAAAAGAACCGGGCGC 4805
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Db 3945 TCGTCCTGCAGTTCATTCAGGGCACCGGACAGGTCCGTCTTGACAAAAGAACCGGGCGC 4004

Qy 4806 CCCTGGCTGCACACGGGGCATCAGAGACGCCGATTGTCGTTGTGTGCCCAG 4865
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Db 4005 CCCTGGCTGCACACGGGGCATCAGAGACGCCGATTGTCGTTGTGTGCCCAG 4064

Qy 4866 TCATAGCCGAATAGCCTCTCCACCCAAGCGGCCGGAGAACCTGCGTGCAATCCATCTTGT 4925
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Db 4065 TCATAGCCGAATAGCCTCTCCACCCAAGCGGCCGGAGAACCTGCGTGCAATCCATCTTGT 4124

Qy 4926 TCAATCATGCGAAACGATCCTCGTCTCTTGATCAGATCTTGATCCCCTGCGCCAT 4985
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Db 4125 TCAATCATGCGAAACGATCCTCATCCTCGTCTCTTGATCCCCTGCGCCAT 4184

Qy 4986 CAG 4988
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Db 4185 CAG 4187

RESULT 7

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Qy 3126 CCATAGGCTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCG 3185
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Db 2526 CCATAGGCTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCG 2585

Qy 3186 AAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTC 3245
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Db 2586 AAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTC 2645

Qy 3246 TCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGT 3305
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2646 TCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGT 2705

Qy 3306 GGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAA 3365
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2706 GGCGCTTTCTCAATGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAA 2765

Qy 3366 GCTGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTA 3425
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2766 GCTGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTA 2825

Qy 3426 TCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAA 3485
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Db 2826 TCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAA 2885

Qy 3486 CAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAA 3545
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Db 2886 CAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAA 2945

Qy 3546 CTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTT 3605
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2946 CTACGGCTACACTAGAAGGACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTT 3005

Qy 3606 CGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTT 3665
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3006 CGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTT 3065

Qy 3666 TTTTGTTTGCAAGCAGCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGAT 3725
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3066 TTTTGTTTGCAAGCAGCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGAT 3125

Qy 3726 CTTTTCTACGGGGTCTGACGCTCAGTGGAACGAAAACTCACGTTAAGGGATTTTGGTCAT 3785
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3126 CTTTTCTACGGGGTCTGACGCTCAGTGGAACGAAAACTCACGTTAAGGGATTTTGGTCAT 3185

Qy 3786 GAGATTATCGTCGACCAAAGCGGCCATCGTGCCTCCCCACTCCTCCAGTTCGGGGGCATG 3845

Db 3186 GAG-- 3188

Qy 3846 GATGCGCCGGATAGCCGCTGCGTCTGGTTTCCTGGATGCCGACGGATTTGCACTGCCGGTAGAA 3905

Db 3189 -- 3188

Qy 3906 CTCCGCGAGTCGTCAGCCTCAGCGAGCAGCCGACCACTCGAACCAACTCGGCCGAGGGGCCCC 3965
          --------------CGGATACATATTTGAATGTATTTAGAAAAATAAACAAATAG
Db 3189 --------------CGGATACATATTTGAATGTATTTAGAAAAATAAACAAATAG 3229

Qy 3966 GGGGGTTGGGCCGAAGAACTCCAGCATGAGATCCCCGGCTGAGGGATCATCCAGCCGGCGTC 4025
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3230 GGGTTCCGCGCACATTTCCCGAAAAGTGCCACCTGTATGCGGTGTGAAATACCGCACAG 3289

Qy 4026 CCGAAAAACGATTCCAAGCCCAACCTTCATAGAAGGCGGCGGTGGAATCTCG 4085
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Db 3290 ATGCGTAAGGAGAAAATACCGCATCAGGAAATTGTAAGCGTTAATAAT------- 3337

Qy 4086 TGAATGGCAGGTTGGGCGTCGGTTCCGTTGGTCGTCATTCGAACCCCAGAGTCCCGCTCAGAAG 4145
          ||||||||||||||||||||||||||||||||||||||||||
Db 3338 --TCCAGAAG 3344

Qy 4146 AACTCGTCAAGAAGGCGATAGAAGGCGATGGCTGCGAATCGGGAGCGGCGGCGGGATACCGTAA 4205
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;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: PatentIn Ver. 2.1
;  SEQ ID NO 2
;  LENGTH: 4293
;  TYPE: DNA
;  ORGANISM: Artificial Sequence
;  FEATURE:
;  OTHER INFORMATION: Description of Artificial Sequence:pMB1-HAMnSOD
;  OTHER INFORMATION: plasmid expression vector
;  FEATURE:
;  NAME/KEY: modified_base
;  LOCATION: (1940)
;  OTHER INFORMATION: n = g, a, c or t
US-10-811-028A-2
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Query Match    32.1%;  Score 1697.8;  DB 21;  Length 4293;
Best Local Similarity  86.7%;  Pred. No. 0;
Matches 1980;  Conservative 0;  Mismatches 102;  Indels 201;  Gaps  2;
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Qy   2706 CTAGACGTAATCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCC 2765
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Db   2212 CTTTGGCGTAATCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCC 2271

Qy   2766 ACACAACATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTA 2825
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2272 ACACAACATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTA 2331

Qy   2826 ACTCACATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCA 2885
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Db   2332 ACTCACATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCA 2391

Qy   2886 GCTGCATTAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTC 2945
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   2946 CGCTTCCTCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGC 3005
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2452 CGCTTCCTCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGC 2511

Qy   3006 TCACTCAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACAT 3065
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Db   2512 TCACTCAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACAT 2571

Qy   3066 GTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTT 3125
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Db   2572 GTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTT 2631

Qy   3126 CCATAGGCTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCG 3185
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2632 CCATAGGCTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCG 2691

Qy   3186 AAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTC 3245
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2692 AAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTC 2751

Qy   3246 TCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGT 3305
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Db   2752 TCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGT 2811

Qy   3306 GGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAA 3365
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2812 GGCGCTTTCTCAATGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAA 2871

Qy   3366 GCTGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTA 3425
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Qy   3426 TCGTCTTGAGTCCAACCCGGTAAGACGACTTATCGCCACTGGCAGCAGCCACTGGTAA 3485
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Db   2932 TCGTCTTGAGTCCAACCCGGTAAGACAGCTTATCGCCACTGGCAGCAGCCACTGGTAA 2991

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Db
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Db   2992 CAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAA 3051
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Qy   3546 CTACGGCTACACTAGAAGGACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTT 3605
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Db   3052 CTACGGCTACACTAGAAGGACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTT 3111

Qy   3606 CGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTT 3665
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Db   3112 CGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTT 3171

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Db   3172 TTTGTTTGCAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGAT 3231

Qy   3726 CTTTTCTACGGGGTCTGACGCTCAGTGGAACGAAAACTCACGTTAAGGGATTTTGGTCAT 3785
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Db   3232 CTTTTCTACGGGGTCTGACGCTCAGTGGAACGAAAACTCACGTTAAGGGATTTTGGTCAT 3291

Qy   3786 GAGATTATCGTCGACCAAAGCGGCCATCGTGCCTCCCCACTCGTCAGTTCGGGGGGCATG 3845
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Db   3292 GAG---------------------------------------------------------- 3294

Qy   3846 GATGGCGCGGATAGCCGCTGCTGTTCCTGGATGCCGACGATTTGCACTGCCGGTAGAA 3905
Db   3295 ------------------------------------------------------------ 3294

Qy   3906 CTCCGCGAGGTCGTCTCCAGCCTCCAGCGACGTGAACCAACTCGCGAGGGGATCGCAGCCC 3965
Db   3295 ------------------------CGGATACATATTTGAATGTATTTAGAAAAATAAACAAATAG 3335

Qy   3966 GGGGTGGGCGAAGAACTCCAGCATGAGATCCCCGCGCTGGAGGATCATCCAGCCGGCGTC 4025
          ||||    |||      |||||||||||| |||   |       |||      ||    |||
Db   3336 GGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGTGTGAAATTGTTATCAGC 3395

Qy   4026 CCGGAAACGATTCCGAAGCCCAACCTTTCATAGAAGGCGGCGGTGAATCGAAATCTCG 4085
          ||||||
Db   3396 ATGCGTAAGGAGAAAATACCGCATCAGGAAATTGTAAGCGTTAATAT------------- 3443

Qy   4086 TGATGGCAGGTTGGGGTGCGGTCATTCGAACCCGGAGTCCCGCTCAGAAG 4145
          |||||||
Db   3444 --------------------------------------------TCAGAAG 3450

Qy   4146 AACTCGTCAAGAAGGCCGATAGAGGCCGATGCGCTGCGAATCGGCGGCGGCGATACCGTAA 4205
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3451 AACTCGTCAAGAAGGCCGATAGAGGCCGATGCGCTGCGAATCGGCGGCGGCGATACCGTAA 3510

Qy   4206 AGCACGAGGAGCGGTCAGCCATTCGCCGCGCCAAGCTCTTCAGCAATATCACGGGTAGCC 4265
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3511 AGCACGAGGAGCGGTCAGCCATTCGCCGCGCCAAGCTCTTCAGCAATATCACGGGTAGCC 3570

Qy   4266 AACGCTATGTCCTGATAGCGGTCCGCCACACCCAGCCGGCCACAGTCGATGAATCCAGAA 4325
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3571 AACGCTATGTCCTGATAGCGGTCCGCCACACCCAGCCGGCCACAGTCGATGAATCCAGAA 3630

Qy   4326 AAGCGGCCATTTTCCACCATGATATTCGGCAAGCAGGCATCGCCATGGGTCACGACGAGA 4385
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3631 AAGCGGCCATTTTCCACCATGATATTCGGCAAGCAGGCATCGCCATGGGTCACGACGAGA 3690

Qy   4386 TCCTCGCCGTCGGGCATGCGCGCCTTGAGCCTGGCGAACAGTTCGGCTGGCGCGAGCCCC 4445
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3691 TCCTCGCCGTCGGGCATGCGCGCCTTGAGCCTGGCGAACAGTTCGGCTGGCGCGAGCCCC 3750

Qy   4446 TGATGCTCTTCGTCCAGATCATCCTGATCGACAAGACCGGCTTCCATCCGAGTACGTGCT 4505
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3751 TGATGCTCTTCGTCCAGATCATCCTGATCGACAAGACCGGCTTCCATCCGAGTACGTGCT 3810

Qy   4506 CGCTCGATGCGATGTTTCGCTTGGTGGTCGAATGGGCAGGTAGCCGGATCAAGCGTATGC 4565
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3811 CGCTCGATGCGATGTTTCGCTTGGTGGTCGAATGGGCAGGTAGCCGGATCAAGCGTATGC 3870

Qy   4566 AGCCGCCGCATTGCATCAGCCATGATGGATACTTTCTCGGCAGGAGCAAGGTGAGATGAC 4625
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3871 AGCCGCCGCATTGCATCAGCCATGATGGATACTTTCTCGGCAGGAGCAAGGTGAGATGAC 3930
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Qy  4626 AGGAGATCTGCCCCGGCCACTTCGCCCAATAGCAGCGCAGTTCCCTTCCCGCTTCCAGTGACA 4685
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3931 AGGAGATCTGCCCCGGCCACTTCGCCCAATAGCAGCGCAGTTCCCTTCCCGCTTCCAGTGACA 3990

Qy  4686 ACGTCGAGCACAGCTGCGCAAGGAACGCCCGTCGTGGCCAGCCACGATAGCCGCGCTGCC 4745
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3991 ACGTCCGAGCACAGCTGCGCAAGGAACGCCCGTCGTGGCCAGCCACGATAGCCGCGCTGCC 4050

Qy  4746 TCGTCTCGAGTTCATTCAGGGCACCGGCACCGGAGCAGGTCGGTCTTGACAAAAGAACCGGCGGC 4805
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4051 TCGTCTTGAGTTCATTCAGGGCACCGGCACCGGAGCAGGTCGGTCTTGACAAAAGAACCGGGCGC 4110

Qy  4806 CCCTGCGCCTGACAGCCCGGAACACGGCGGCGCATCAGAGCAGCCAGTTGTCTGTTGTGCCCAG 4865
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4111 CCCTGCGCCTGACAGCCCGGAACACGGGCGGCGCATCAGAGCAGCCAGTTGTCTGTTGTGCCCAG 4170

Qy  4866 TCATAGCCGAATAGCCTCTCCACCCAAGCCGGCCGGAGAACCTGCGTGCAATCCATCTTGT 4925
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4171 TCATAGCCGAATAGCCTCTCCACCCAAGCCGGCCGGAGAACCTGCGTGCAATCCATCTTGT 4230

Qy  4926 TCAATCATGCGGAAACGATCTCCATCCTGTCTCTTGATCAGATCTTGATCCCCTGCGCCAT 4985
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4231 TCAATCATGCGGAAACGATCTCCATCCTGTCTCTTGATCAGAGCTTGATCCCCTGCGCCAT 4290

Qy  4986 CAG 4988
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Db  4291 CAG 4293
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RESULT 8
US-10-811-028A-1
; Sequence 1, Application US/10811028A
; Publication No. US2005043258A1
; GENERAL INFORMATION:
;   APPLICANT: Bennett, Michael
;   APPLICANT: Chen, Yen-Ju
;   APPLICANT: Genteric, Inc.
;   TITLE OF INVENTION: Methods of Treating Xerostomia and Xerophthalmia
;   FILE REFERENCE: 020714-0024210US
;   CURRENT APPLICATION NUMBER: US/10/811,028A
;   CURRENT FILING DATE: 2004-03-25
;   PRIOR APPLICATION NUMBER: US 60/458,793
;   PRIOR FILING DATE: 2003-03-26
;   NUMBER OF SEQ ID NOS: 11
;   SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 4332
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:pMB1-MnSOD
;   OTHER INFORMATION: plasmid expression vector
;   FEATURE:
;   NAME/KEY: modified_base
;   LOCATION: (1979)
;   OTHER INFORMATION: n = g, a, c or t
US-10-811-028A-1

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Query Match     32.1%;  Score 1697.8;  DB 21;  Length 4332;
Best Local Similarity   86.7%;  Pred. No. 0;
Matches 1980;  Conservative   0;  Mismatches 102;  Indels 201;  Gaps   2;

Qy  2706 CTAGACGTAATCATGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCC 2765
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2251 CTTGGCGTAATCATGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCC 2310

Qy  2766 ACACAACATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTA 2825
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2311 ACACAACATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTA 2370

Qy  2826 ACTCACATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCA 2885
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Db  3374 ...
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Db  2371 ACTCACATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCA 2430

Qy  2886 GCTGCATTAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTC 2945
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2431 GCTGCATTAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTC 2490

Qy  2946 CGCTTCCTCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGC 3005
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2491 CGCTTCCTCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGC 2550

Qy  3006 TCACTCAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACAT 3065
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2551 TCACTCAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACAT 2610

Qy  3066 GTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTT 3125
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2611 GTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTT 2670

Qy  3126 CCATAGGCTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCG 3185
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2671 CCATAGGCTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCG 2730

Qy  3186 AAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTC 3245
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2731 AAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTC 2790

Qy  3246 TCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGT 3305
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2791 TCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGT 2850

Qy  3306 GGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAA 3365
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2851 GGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAA 2910

Qy  3366 GCTGGGCTGTGTGCACGAACCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTA 3425
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2911 GCTGGGCTGTGTGCACGAACCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTA 2970

Qy  3426 TCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAA 3485
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2971 TCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAA 3030

Qy  3486 CAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAA 3545
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3031 CAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAA 3090

Qy  3546 CTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTT 3605
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3091 CTACGGCTACACTAGAAGGACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTT 3150

Qy  3606 CGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTT 3665
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3151 CGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTT 3210

Qy  3666 TTTTGTTTGCAAGCAGCAGATTACGGCGCAGATTACGGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGAT 3725
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3211 TTTTGTTTGCAAGCAGCAGATTACGGCGCAGATTACGGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGAT 3270

Qy  3726 CTTTTCTACGGGGTCTGACGCTCAGTGGAACGAAAACTCACGTTAAGGGATTTTGGTCAT 3785
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3271 CTTTTCTACGGGGTCTGACGCTCAGTGGAACGAAAACTCACGTTAAGGGATTTTGGTCAT 3330

Qy  3786 GAGATTATCGTCGACCAAAGCGGCCATCGTGCCTCCCCACTCGTGCTGGGGGCATG 3845
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Db  3331 GAG 3333

Qy  3846 GATGCGCGGATAGCCGCTGCGTTGGTTTCCTGATGCGGTATTTCTCCTTACGCATCTGTGCGGTAGAA 3905
Db  3334 ---

Qy  3906 CTCCGCGAGGTCGTCGAGCCTCAGCGCCAGCGGTGATCAGCCTGAACCAACTCGCGAGGGGATCGAGCCCC 3965
Db       CCGGATACATATTTGAATGTATTTAGAAAAATAAACAAATAG 3374
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RESULT 9
US-10-811-028A-3
; Sequence 3, Application US/10811028A
; Publication No. US2005004325BA1
; GENERAL INFORMATION:
;   APPLICANT: Bennett, Michael
;   APPLICANT: Chen, Yen-Ju
;   APPLICANT: Genteric, Inc.
;   TITLE OF INVENTION: Methods of Treating Xerostomia and Xerophthalmia
;   FILE REFERENCE: 020714-002410US
;   CURRENT APPLICATION NUMBER: US/10/811,028A
;   CURRENT FILING DATE: 2004-03-25
;   PRIOR APPLICATION NUMBER: US 60/458,793
;   PRIOR FILING DATE: 2003-03-26
;   NUMBER OF SEQ ID NOS: 11
;   SOFTWARE: PatentIn Ver. 2.1
;
; SEQ ID NO 3
;   LENGTH: 5753
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:pMB1-CAT
;   OTHER INFORMATION: plasmid expression vector
US-10-811-028A-3

Query Match   32.1%;   Score 1697.8;   DB 21;   Length 5753;
Best Local Similarity   86.7%;   Pred. No. 0;
Matches 1980;   Conservative   0;   Mismatches   102;   Indels 201;   Gaps   2;

Qy   3966 GGGGTGGGCGAAGAACTCCAGCATGAGATCCCCGCCTGGAGGATCATCCAGCCGGCGTC 4025
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Db   3375 GGGTTCCGCGCCACATTTCCCGAAAAGTGCCACCTGTATGCGGGTGTGTCGAAAATCTCG 3434

Qy   4026 CCGGAAAACGATTCCGAAGCCCAACCTTTCATAGAGAAGGCGGGGTGAATCGAAAATCTCG 4085
          ||| ||| |||
Db   3435 ATGCGTAAGGAGAAAAATACCGCATCAGAGAAATTGTAAGCGTTAATAAT----------- 3482

Qy   4086 TGATGGCAGGTTGGGCGTCGGTGGTCGGTCATTTCGAACCCCAGAGTCCGCTCAGAAG 4145
                                                         ||||||
Db   3483 --TCAGAAG 3489

Qy   4146 AACTCGTCAAGAAGGCGATAGAAGGGCGATGCCTGCGAATCGGGAGGCGGCGGATACCGTAA 4205
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3490 AACTCGTCAAGAAGGCGATAGAAGGGCGATGCGCTGCGAATCGGGAGGCGGCGGATACCGTAA 3549

Qy   4206 AGCACAGGAGGAAGCGGTCAGCCCATTCGCCGCCAAGCTCTTCAGCAATATCACGGGTAGCC 4265
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3550 AGCACAGGAGGAAGCGGTCAGCCCATTCGCCGCCAAGCTCTTCAGCAATATCACGGGTAGCC 3609

Qy   4266 AACGCTATGTCCTGATAGCGGTCCGCCAACCCAGCCGGCCACAGTCGATGAATCCAGAA 4325
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3610 AACGCTATGTCCTGATAGCGGTCCGCCAACCCAGCCGGCCACAGTCGATGAATCCAGAA 3669

Qy   4326 AAGCGGCCATTTTCCACCATGATATTCGGCAAGCAGGCATCGCCATGGGTCACGACGAGA 4385
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3670 AAGCGGCCATTTTCCACCATGATATTCGGCAAGCAGGCATCGCCATGGGTCACGACGAGA 3729

Qy   4386 TCCTCGCCGTCGGGCATGCGCGCCTTGAGCCTGGCGAACAGTTCGGCTGGCGCGAGCCCC 4445
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3730 TCCTCGCCGTCGGGCATGCGCGCCTTGAGCCTGGCGAACAGTTCGGCTGGCGCGAGCCCC 3789

Qy   4446 TGATGCTCTTCGTCCAGATCATCGTCGACAAGACCGGCTTCATCCGAGTACGTGCT 4505
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3790 TGATGCTCTTCGTCCAGATCATCCGAGATCATCGTCGACAAGACCGGCTTCCATCCGAGTACGTGCT 3849

Qy   4506 CGCTCGATGCGATGTTTCGCTTGGTTGGTCGAATGGGTCAGGTAGCCGGATCAAGCGTATGC 4565
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db   3850 CGCTCGATGCGATGTTTCGCTTGGTTGGTCGAATGGGTCAGGTAGCCGGATCAAGCGTATGC 3909

Qy   4566 AGCCGCCGCATTGCATCAGCCATGATGGATACTTTCTCGGCAGGAGCAAGGTGAGATGAC 4625
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3910 AGCCGCCGCATTGCATCAGCCATGATGGATACTTTCTCGGCAGGAGCAAGGTGAGATGAC 3969

Qy   4626 AGGAGATCTGCCCCGGCACTTCGCCCAATAGCAGCCAGTCCCTTCCGCTTCCTTCAGTGACA 4685
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3970 AGGAGATCTGCCCCGGCACTTCGCCCAATAGCAGCCAGTCCCTTCCCGCTTCCTTCAGTGACA 4029

Qy   4686 ACGTCGAGCACAGCTGCGCAAGGAACGCCCGTCGTGCCCAGCACGATAGCCGCGCTGCC 4745
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db   4030 ACGTCGAGCACAGCTGCGCAAGGAACGCCCGTCGTGCCCAGCACCGATAGCCGCGCTGCC 4089

Qy   4746 TCGTTCCTGCAGTTCATTCAGGGCACCGGACAGCTCGTCTTGACAAAAAGAACCGGCGC 4805
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db   4090 TCGTTCTTGCAGTTCATTCAGGGCACCGGACAGCTCGTCTTGACAAAAAGAACCGGGCGC 4149

Qy   4806 CCCTGCGCTGACAGCCGGAACACGGGCGGCCATCAGACGGGCCAGCCGATTCGTGTTGTGCCCAG 4865
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Db   4150 CCCTGCGCTGACAGCCGGAACACGGGCGGCCATCAGACGGGCCAGCCGATTGTCTGTTGTGCCCAG 4209

Qy   4866 TCAATAGCCGAATAGCCTTCTCCACCCAAGCGGCCGGAGAACCTGCGTGCAATCCATCTTGT 4925
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Db   4210 AAACCCGACACAGGACTATAAAGATACCAGGCGTTTCCCCTGGAAGCTCCCTCGTGCGCTC 4269

Qy   4926 TCAATAGCCGAAAACGATCCTCATCCTGTCTTGATCAGATCTTGATCCATCTTGT 4985
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4270 TCAATAGCCGAAAACGATCCTCATCCTGTCTTGATCAGAGCTTGATCCATCTTGT 4329

Qy   4986 CAG 4988
          |||
Db   4330 CAG 4332

Qy   2706 CTAGACGTAATCATGTCATAGCTGTTCCTGTGTGAAATTGTATCCGCTCACAATTCC 2765
          ||| ||||||||||||||||||||||||||||||||
Db   3672 CTTGGGTAATCATGTCATAGCTGTTCCTGTGTGAAATTGTATCCGCTCACAATTCC 3731

Qy   2766 ACACAACATACGAGCGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTA 2825
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3732 ACACAACATACGAGCGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTA 3791

Qy   2826 ACTCACATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCA 2885
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3792 ACTCACATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCA 3851

Qy   2886 GCTGCATTAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTC 2945
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3852 GCTGCATTAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTC 3911

Qy   2946 CGCTTCCTCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGC 3005
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3912 CGCTTCCTCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGC 3971

Qy   3006 TCACTCAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACAT 3065
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3972 TCACTCAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACAT 4031

Qy   3066 GTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTT 3125
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4032 GTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTT 4091

Qy   3126 CCATAGGCTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCG 3185
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4092 CCATAGGCTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCG 4151

Qy   3186 AAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCTGGAAGCTCCCTCGTGCGCTC 3245
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Db   4152 AAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCTGGAAGCTCCCTCGTGCGCTC 4211

Qy   3246 TCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGT 3305
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4212 TCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGT 4271

Qy   3306 GGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAA 3365
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4272 GGCGCTTTCTCAATGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAA 4331

RESULT 10
US-10-811-028A-4

; Sequence 4, Application US/10811028A
; Publication No. US2005004325BA1
; GENERAL INFORMATION:
;   APPLICANT: Bennett, Michael
;   APPLICANT: Chen, Yen-Ju
;   APPLICANT: Genteric, Inc.
;   TITLE OF INVENTION: Methods of Treating Xerostomia and Xerophthalmia
;   FILE REFERENCE: 020714-002410US
;   CURRENT APPLICATION NUMBER: US/10/811,028A
;   CURRENT FILING DATE: 2004-03-25
;   PRIOR APPLICATION NUMBER: US 60/458,793
;   PRIOR FILING DATE: 2003-03-26
;   NUMBER OF SEQ ID NOS: 11
;   SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
;   LENGTH: 5760
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:pMB1-Mt-CAT
;   OTHER INFORMATION: plasmid expression vector
US-10-811-028A-4

Query Match   32.1%;   Score 1697.8;   DB 21;   Length 5760;
Best Local Similarity   86.7%;   Pred. No. 0;
Matches 1980;   Conservative   0;   Mismatches 102;   Indels 201;   Gaps 2;

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Qy   3846 GATGCGCGGATAGCGCGCTGCTCGGTTCCTGGATGCCGACGGATTTGCACTGCCGGTAGAA 3905
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4762 ------------------------------------------------------------ 4761

Qy   3906 CTTCCGCGAGGTCGTCCAGCCTCAGGCAGCAGCAGTGAACCAACTCGCGAGGGGATCGAGCCC 3965
          ||||||||||||||||||||||||         ||||||||||||||||||||||||||||
Db   4762 ------------CGGATACATATTTGAATGTATTTAGAAAAATAAACAAATAG 4802

Qy   3966 GGGGTGGCGAAGAACTCCAGACATGAGATCCCGCGCTGGAGGATCATCCAGCCGGCCGTC 4025
          ||||   ||||||||||||||         |||||||||||||         
Db   4803 GGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGTATGCGGTGTGAAATACCGCACAG 4862

Qy   4026 CCGGAAAACGATTCCGAAGCCCAACCTTTCATAGAAGGCGGCCGGTGGAATCGAAATCTCG 4085
          |||||         |||         ||      ||
Db   4863 ATGCGTAAGGAGAAAATACCGCATCAGGAAATTGTAAGCGTTAATAAT------------ 4910

Qy   4086 TGATGGCAGGTTGGGCGTCGCTTGGTCGGTCATTCGAACCCCAGAGTCCCGCTCAGAAG 4145
          |||                         ||||
Db   4911 ------------------------------------------------TCAGAAG 4917

Qy   4146 AACTCGTCAAGAAGGCGGATAGAAGGCCATGCGCTGCGAATCGGGAGCCGCGATACCGTAA 4205
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4918 AACTCGTCAAGAAGGCGGATAGAAGGCCATGCGCTGCCGAATCGGGAGCGGCGATACCGTAA 4977

Qy   4206 AGCACGAGGAAGCCGGTCAGCCGCCCATTCGCCGCCCAAGCTCTTCAGCAATATCACGGTAGCC 4265
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4978 AGCACGAGGAAGCCGGTCAGCCGCCCATTCGCCGCCCAAGCTCTTCAGCAATATCACGGTAGCC 5037

Qy   4266 AACGCTATGTCCTGATAGCGGTTCCGCCACACCCAGCCGGCCACAGTCGATGAATCCAGAA 4325
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5038 AACGCTATGTCCTGATAGCGGTTCCGCCACACCCAGCCGGCCACAGTCGATGAATCCAGAA 5097

Qy   4326 AAGCCGGCCATTTTCCACCATGATAATTCGGCAGCAGCAGCATCGGTCACGACGAGA 4385
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5098 AAGCCGGCCATTTTCCACCATGATAATTCGGCAGCAGCAGCATCGGTCACGACGAGA 5157

Qy   4386 TCCTCGCGCGTCGGCGCATGCGCCCTTGAGCCTTCGGGCGACAGTTCGGCGTGGCGGAGCCCC 4445
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5158 TCCTCGCGCGTCGGCGCATGCGCCCTCGCGCGTCGGCGCATGCGCCCTCGGGCTGGCGGAGCCCC 5217

Qy   4446 TGATGCTCTTCGTCCGATCATCCTGATCGACAAGACCGGCTTCCATCCGAGTACGTGCT 4505
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5218 TGATGCTCTTCGTCCGATCATCCTGATCGACAAGACCGGCTTCCATCCGAGTACGTGCT 5277

Qy   4506 CGCTCGATGCGATGTTTCGCTTCGGTGGTCGTGAATGGGCAGGAGTAGCGTATGC 4565
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5278 CGCTCGATGCGATGTTTCGCTTCGGTGGTCGTGAATGGGCAGGAGTAGCCGTATGC 5337

Qy   4566 AGCCGCCGCATTGCATCAGCAATGATACTTTCTCGGCAGGAGCAAGGTGAGATGAC 4625
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5338 AGCCGCCGCATTGCATCAGCAATGATACTTTCTCGGCAGGAGCAAGGTGAGATGAC 5397

Qy   4626 AGGAGATCCTGCCCGGCACTTCGCCCAATAGCAGCCAGTCCCTTCCGCTTCAGTGACA 4685
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5398 AGGAGATCCTGCCCGGCACTTCGCCCAATAGCAGCCAGTCCCTTCCGCTTCAGTGACA 5457

Qy   4686 ACGTCGAGCACAGCGGCCAACGAACCGCCCGTGCGCCAGCAGGAACGGCCGTATGCC 4745
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5458 ACGTCGAGCACAGCGGCCAACGAACCGCCCGTGCGCCAGCAGGAACGGCCGTCGTGCC 5517

Qy   4746 TCGTCCTGCAGTTCATTCAGGGCACCGGACAGTCGTCTTGACAAAAAGAACCGGGGGC 4805
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5518 TCGTCTTGCAGTTCATTCAGGGCACCGGACAGTCGTCTTGACAAAAAGAACCGGGGC 5577

Qy   4806 CCCTGGCTGACAGCGGAACGCGGCGGCATCAGAGCACCGATTGTCTGTTGTGCCCCAG 4865
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5578 CCCTGGCTGACAGCGGAACGCGGCGGCATCAGAGCACGGATTGTCTGTTGTGCCCCAG 5637

Qy   4866 TCATAGCCGAATAGCCTTCTCCACCCAAGCGGCCGAGAACCTGCGTGCAATCCATCTTGT 4925
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5638 TCATAGCCGAATAGCCTTCTCCACCCAAGCGGCCGAGAACCTGCGTGCAATCCATCTTGT 5697

Qy   4926 TCAATCATGCGAAACGATCCTCATCCTGTCTCTTGATCAGATCTTGATCCCGTGCCGCCAT 4985
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Qy   2766 ACACAACATACGAGCCGGAAGCATAAAGTGTAAAGCCTTAATGAGTGAGCTA 2825
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3739 ACACAACATACGAGCCGGAAGCATAAAGTGTAAAGCCTTAATGAGTGAGCTA 3798

Qy   2826 ACTCACATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCA 2885
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3799 ACTCACATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCA 3858

Qy   2886 GCTGCATTAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTC 2945
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3859 GCTGCATTAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTC 3918

Qy   2946 CGCTTCCTCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGC 3005
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3919 CGCTTCCTCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGC 3978

Qy   3006 TCACTCAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACAT 3065
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3979 TCACTCAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACAT 4038

Qy   3066 GTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTT 3125
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4039 GTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTT 4098

Qy   3126 CCATAGGCTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCG 3185
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4099 CCATAGGCTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCG 4158

Qy   3186 AAACCCGACAGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTC 3245
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4159 AAACCCGACAGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTC 4218

Qy   3246 TCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGT 3305
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4219 TCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGT 4278

Qy   3306 GGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAA 3365
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4279 GGCGCTTTCTCAATGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAA 4338

Qy   3366 GCTGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTA 3425
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4339 GCTGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTA 4398

Qy   3426 TCGTCTTGAGTCCAACCCGGTAAGACAGACTTATCGCCACTGGCAGCAGCCACTGGTAA 3485
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4399 TCGTCTTGAGTCCAACCCGGTAAGACAGACTTATCGCCACTGGCAGCAGCCACTGGTAA 4458

Qy   3486 CAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAA 3545
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4459 CAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAA 4518

Qy   3546 CTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTT 3605
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4519 CTACGGCTACACTAGAAGGACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTT 4578

Qy   3606 CGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTT 3665
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4579 CGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTT 4638

Qy   3666 TTTTGTTTGCAAGCAGCAGATTACGGCGCAGATTACGGCGCAGAAAAAGGATCTCAAGAAGATCCTTTGAT 3725
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4639 TTTTGTTTGCAAGCAGCAGATTACGGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGAT 4698

Qy   3726 CTTTTCTACGGGGTCTGACGCTCAGTGGAACGAAAACTCACGTTAAGGGATTTTGGTCAT 3785
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4699 CTTTTCTACGGGGTCTGACGCTCAGTGGAACGAAAACTCACGTTAAGGGATTTTGGTCAT 4758

Qy   3786 GAGATTATCGTCGACCAAAGCGGCCATCGTGCCTCCCCACTCGCAGTTCGGGGGCATG 3845
          |||
Db   4759 GAG------------------------------------------------ 4761
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Db   5698 TCAATCATGCGAAACGATCCTCATCCTGTCTTCTGATCAGAGCTTGATCCCCTGCGCCAT 5757

Qy   4986 CAG 4988

Db   5758 CAG 5760

RESULT 11
US-10-286-186-16/c
; Sequence 16, Application US/10286186
; Publication No. US20030143741A1
; GENERAL INFORMATION:
; APPLICANT: PALMER, KENNETH E.
; APPLICANT: POGUE, GARY P.
; TITLE OF INVENTION: ROLLING CIRCLE REPLICON EXPRESSION
; TITLE OF INVENTION: VECTOR
; FILE REFERENCE: 0080101790US00
; CURRENT APPLICATION NUMBER: US/10/286,186
; CURRENT FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: US/09/505,477
; PRIOR FILING DATE: 2000-02-16
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 5225
; TYPE: DNA
; ORGANISM: Porcine Circovirus
US-10-286-186-16

Query Match   32.0%;   Score 1692.4;   DB 15;   Length 5225;
Best Local Similarity 82.7%;   Pred. No. 0;
Matches 2087;   Conservative 0;   Mismatches 206;   Indels 231;   Gaps 4;

Qy   2942 CTTCCGCTTCCTCGCTCACTGACTCGGTCGTTGCGCTGGCTGCGGCGGCGGAGCGGGTAT 3001
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5225 CTTCCGCTTCCTCGCTCACTGACTCGGTCGTTGCGCTGGCTGCGGCGGCGGAGCGGGTAT 5166

Qy   3002 CAGCTTCACTCACTCAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGA 3061
           ||||||||||||||||||||||||||||||||||| |||||||||||| ||| |||||||||
Db   5165 CAGCTTCACTCAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGA 5106

Qy   3062 ACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGT 3121
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5105 ACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCCGTAAAAAGGCCGCGTTGCTGGCGT 5046

Qy   3122 TTTTCCATAGGCTCCGCCCCCCTGACGAGCATCACAAAAATCGACGGCTCAAGTCAGAGGT 3181
           |||||||||||||||||||||||||||||||||||||| |||||||||||||||||||||
Db   5045 TTTTCCATAGGCTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGT 4986

Qy   3182 GGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGC 3241
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4985 GGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGC 4926

Qy   3242 GCTCTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAA 3301
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4925 GCTCTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAA 4866

Qy   3302 GCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCT 3361
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4865 GCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCT 4806

Qy   3362 CCAAGCTGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTA 3421
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3725 GAGGAAGCCGGTCAGCCCGGTTCAGCCCGACTTCGCCGCCCACAGCTCTTCAGCCCACTG 3666

Qy   3422 ACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTG 3481
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4745 ACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTG 4686

Qy   3482 GTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGC 3541
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4685 GTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGC 4626

Db   3542 CTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCGCGCTCTGCTGAAGCCAGTTA 3601
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4625 CTAACTACGGCTACACTAGAAGGACAGTATTTGGTATCGCGCTCTGCTGAAGCCAGTTA 4566

Db   3602 CCTTCGGAAAAAGAGTTGGTAGCTCTTGATCGGCAAACAACAACCACCGCTGGTAGCGGTG 3661
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4565 CCTTCGGAAAAAGAGTTGGTAGCTCTTGATCGGCAAACAACAACCACCGCTGGTAGCGGTG 4506

Qy   3662 GTTTTTTTGTTTGCAAGCAGCAGATTACGGCGCAGAAAAAAAGGATCTCAAGAAGATCCTT 3721
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4505 GTTTTTTTGTTTGCAAGCAGCAGATTACGGCGCAGAAAAAAAGGATCTCAAGGATTTTGG 4446

Qy   3722 TGATCTTTTCTACGGGGTCTGACGCTCAGTGGAACGAAAACTCACGTTAAGGGATTTTGG 3781
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4445 TGATCTTTTCTACGGGGTCTGACGCTCAGTGGAACGAAAACTCACGTTAAGGGATTTTGG 4386

Qy   3782 TCATGAGATTATC--- 3794
           ||||||||||||||
Db   4385 TCATGAGATTATCAAAAAGGATCTTCACCTAGATCCTTTTAAATTAAAAATGAAGTTTTA 4326

Qy   3795 --GTCGACCA 3802
                                                       ||||||||
Db   4325 GCACGTGTCAGTCCTGCTCCTCGGGCCACGAGTGACGCAGTTGCCGGCGCCGGGTCGCGCA 4266

Qy   3803 AAGCGGCCATCGTGCTGCTCCCCACTCCTGCAGTTCGGGGGCATGGATGCGCGGATAGCCGC 3862
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4265 GGGCGAACTCCCGCCCCCACGCGGCTGCTCGGCCGATCTCGGTCAGCTGCATCGTCATGGATGCGCGGATAGCCGC 4206

Qy   3863 TGCTGGTTCCTCTGGATGCCGACGATTGCACTGCCGGTAGAACTCCGCGAGGTCGTCCA 3922
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4205 CCCGGAAGTTCGTGGACACGACCTCCGACCACTCGGCGTACAGCTCGTCCAGGCCGCCGCA 4146

Qy   3923 GCC--- 3925
           |||
Db   4145 CCCACACCCAGGGCCAGGGTCGTTGTCCGGCACCACCTGGTCCTGGACCGCGTGATGAACA 4086

Qy   3926 ---TCAGGCAGCAGCTGAACCAACTGCGAGGCGGGGATCGAACTCGGTGGGCGAAGAACT 3982
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4085 GGGTTCACGTCGTCCCGGACCACGACGCGAGTCGTCTCCAGCGAGTCCCGGGAGACC 4026

Qy   3983 -----------------------AGATCCCGCTGCGACGATCATCCGGCGTC 4025
                                  ||||||||||||||||||||||||||
Db   4025 CGAGCCTGGTCAACTTGGCCATGGCCCCTCCACGTGCTATTATTGAAGCATTTATC 3966

Qy   4026 CCGGAAAACGATTCCGAAGCCCAACCTTTCATGAGAGGCGGCGGCGTGAATCGAAATCTCG 4085
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3965 AGGGTTATTGTCTCATGAGCGGATACATATTGATGAATGTATTGTTAGAAAAATAAACAAATAG 3906

Qy   4086 TGATGGCAGGTTGGGCGTGCTTGGTCGGTCATTTCGAACCCCAGAGTCCGC------ 4138
           ||||||||||||||||||||||||||||||||||||||||||||||||
Db   3905 GGGTTCGGCGACATTTCCCGAAAAGTGCCACCTGTATGCGGTGTGAAATACCGCACAG 3846

Qy   4139 -----------------------------TCAGAAGAACTC 4150
                                       ||||||||||||
Db   3845 ATGCGTAAGGAGAAAATACCGCATCAGGAGAAATTGTAAGCGTTAATAATTCAGAAGAACTC 3786

Qy   4151 GTCAAGAAGGCGGATAGAAGGCGGATGCGCTGCGAAATCGGGAGCGGCGGATACCGTAAAGCAC 4210
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3785 GTCAAGAAGGCGGATAGAAGGCGGATGCGCTGCGAATCGGGAGCGGCGGATACCGTAAAGCAC 3726

Qy   4211 GAGGAAGCGGTCAGCCCATTGCCGCCGCCAAGTCTTCAGCAATATCACGGGGTAGCCAACGC 4270
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3725 GAGGAAGCGGTCAGCCCATTGCCGCCGCCAAGTCTTCAGCAATATCACGGGGTAGCCAACGC 3666

Qy   4271 TATGTCCTGATAGCGGTCCGCCAGCGTGACCGGGCCATGGCGCAGCGACCACTG 4330
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3665 TATGTCCTGATAGCGGTCCGCCAGCGTGACCGGGCCATGGCGCAGCGACCACTG 3606

Qy   4331 GCCATTTTCCACCATGATAGTTCGGCAACGATGGCCTCCATGGTCACGACGATCCTC 4390
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3605 GCCATTTTCCACCATGATATTCGGCAACGATGGCCTCCATGGTCACGACGACATCCTC 3546

; SEQ ID NO 10
; LENGTH: 6233
; TYPE: DNA
; ORGANISM: Plasmid pCR-XL-TOPO-CMV-pur-attB
US-10-790-455-10

Query Match   30.9%;   Score 1634.4;   DB 20;   Length 6233;
Best Local Similarity   80.6%;   Pred. No. 0;
Matches 2082;   Conservative   0;   Mismatches 211;   Indels 291;   Gaps 3;

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Qy    4391 GCCGTCGGGCATGCGCGCCTTGGCGAACAGTTCGGCTGCGGCTGGGCGGCGAGCCCCTGATG 4450
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3545 GCCGTCGGGCATGCTCGCGCCTTGAGCCTTGAGCCTTGGCGAACAGTTCGGCTGCGGCTGGGCGGCGAGCCCCTGATG 3486

Qy    4451 CTCTTCGTCCAGATCATCCTGATCGACAAGACCGGCTTCATCCGAGTACGTCGCTCCGCTC 4510
           |||||||||||||||||||||||||||||||||||||||||||||
Db    3485 CTCTTCGTCCAGATCATCCTGATCGACAAGACCGGCTTCATCCGAGTACGTCGCTCCGCTC 3426

Qy    4511 GATGCCGATGTTTCGGTTGGTGGTCGAATGGGCAGTAGCCGGATCAAGCGTATGCAGCCG 4570
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3425 GATGCCGATGTTTCGGTTGGTGGTCGAATGGGCAGTAGCCGGATCAAGCGTATGCAGCCG 3366   Db 3001

Qy    4571 CCGCATTGCATCAGCCATGATGATACTTTCTCGGCAGGAGCAAGTGAGATGACAGGAG 4630
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3365 CCGCATTGCATCAGCCATGATGATACTTTCTCGGCAGGAGCAAGTGAGATGACAGGAG 3306   Db 6174

Qy    4631 ATCCTGCCCCCGGCCACTTCGCCCAATAGCAGCCAGTCCCTTCGGCGCTCCAGTGACAACGTC 4690
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3305 ATCCTGCCCCCGGCCACTTCGCCCAATAGCAGCCAGTCCCTTCGGCGCTCCAGTGACAACGTC 3246   Db 6114

Qy    4691 GAGCACAGCTGCGCAAGGAACGCCCGTCGTGCCAGCCACGATAGCCGCGCTGCCTCGTC 4750
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3245 GAGCACAGCTGCGCAAGGAACGCCCGTCGTGCCAGCCACGATAGCCGCGCTGCCTCGTC 3186   Db 6054

Qy    4751 CTGCAGTTCATTCAGGGCACCGGACAGGTCGGTCTTGACAAAAGAACCGGGCGCCCCTG 4810
           |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3185 TTGCAGTTCATTCAGGGCACCGGACAGGTCGGTCTTGACAAAAGAACCGGGCGCCCCTG 3126   Db 5994

Qy    4811 CGCTGACAGCCGGAACACGGCCGGCGGCATCAGAGCAGCCGATTGTCTGTTGTGCCCAGTCATA 4870
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3125 CGCTGACAGCCGGAACACGGCCGGCGGCATCAGAGCAGCCGATTGTCTGTTGTGCCCAGTCATA 3066   Db 5934

Qy    4871 GCCGAATAGCCTCTCCACCCAGCGGCCGGAGAACCTGCGTGCAATCCATCTTGTTCAAT 4930
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3065 GCCGAATAGCCTCTCCACCCAGCGGCCGGAGAACCTGCGTGCAATCCATCTTGTTCAAT 3006   Db 5874

Qy    4931 CATGCCGAAACGATCTCCATCCTGTCTCTTGATCAGATCTTGATCCCTGCGGCCATCAGAT 4990
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3005 CATGCCGAAACGATCTCCATCCTGTCTCTTGATCAGATCTTGATCCCTGCGGCCATCAGAT 2946   Db 3421

Qy    4991 CCTTGGCGGCAAGAAAGCCATCAGTTACTTGCAGGGCTTCGAGGGTTCCCAACCTTACCAGAGGG 5050
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2945 CCTTGGCGGCGAGAAAGCCATCAGTTACTTGCAGGGCTTCGAGGGTTCCCAACCTTACCAGAGGG 2886   Db 5754

Qy    5051 CGCCCCAGCTGCAATTCCGGTTCGCTTGCTGTCGTCCATAAAACCGCCCAGTCTAGCTATCG 5110
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2885 CGCCCCAGCTGCAATTCCGGTTCGCTTGCTGTCGTCCATAAAACCGCCCAGTCTAGCTATCG 2826   Db 3481

Qy    5111 CCATGTAAGCCCACTGCAAGCTACCTGCTTTCTCTTTGCGCTTGCGTTTTCCCTTGTCCA 5170
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2825 CCATGTAAGCCCACTGCAAGCTACCTGCTTTCTCTTTGCGCTTGCGTTTTCCCTTGTCCA 2766   Db 5694

Qy    5171 GATAGCCCAGTAGCTGACATTCATCCGGGGTCAGCACCGTTTCTGCGGACTGGCTTTCTA 5230
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2765 GATAGCCCAGTAGCTGACATTCATCCGGGGTCAGCACCGTTTCTGCGGACTGGCTTTCTA 2706   Db 5574

Qy    5231 CGTG 5234
           ||||
Db    2705 CGTG 2702                                                              Db 3661
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(continued)

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Qy    2942 CTTCCGCTTCCTCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTAT 3001
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    6233 CTTCCGCTTCCTCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTAT 6174

Qy    3002 CAGCTCACTCAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGA 3061
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    6173 CAGCTCACTCAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGA 6114

Qy    3062 ACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGT 3121
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    6113 ACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGT 6054

Qy    3122 TTTTCCATAGGCTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGT 3181
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    6053 TTTTCCATAGGCTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGT 5994

Qy    3182 GGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGC 3241
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5993 GGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGC 5934

Qy    3242 GCTCTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAA 3301
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5933 GCTCTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAA 5874

Qy    3302 GCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCT 3361
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Db    5873 GCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCT 5814

Qy    3362 CCAAGCTGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTA 3421
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5813 CCAAGCTGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTA 5754

Qy    3422 ACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTG 3481
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5753 ACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTG 5694

Qy    3482 GTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGC 3541
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Db    5693 GTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGC 5634

Qy    3542 CTAACTACGGCTACACTAGAAGGACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTA 3601
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5633 CTAACTACGGCTACACTAGAAGGACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTA 5574

Qy    3602 CCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTG 3661
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5573 CCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTG 5514

Qy    3662 GTTTTTTTGTTTGCAAGCAGCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTT 3721
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5513 GTTTTTTTGTTTGCAAGCAGCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTT 5454

Qy    3722 TGATCTTTTCTACGGGGTCTGACGCTCAGTGGAACGAAAACTCACGTTAAGGGATTTTGG 3781
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5453 TGATCTTTTCTACGGGGTCTGACGCTCAGTGGAACGAAAACTCACGTTAAGGGATTTTGG 5394

Qy    3782 TCATGAGATTATC----------------------------------------------- 3794
           |||||||||||||
Db    5393 TCATGAGATTATCAAAAAGGATCTTCACCTAGATCCTTTTAAATTAAAAATGAAGTTTTA 5334

Qy    3795 ---------------------------------------GTCGACCA 3802
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Db    5333 GCACGTGTCAGTCCTGCTCCTCGGCCACGAAGTGCACGCAGTTGCCGGCCGTCCGCGCA 5274
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RESULT 12
US-10-790-455-10/c
; Sequence 10, Application US/10790455
; Publication No. US20040210954A1
GENERAL INFORMATION:
;   APPLICANT: AviGenics, Inc
;   TITLE OF INVENTION: Avian Integrase-mediated Transformation
;   FILE REFERENCE: A181 1080.1
;   CURRENT APPLICATION NUMBER: US/10/790,455
;   CURRENT FILING DATE: 2004-03-01
;   NUMBER OF SEQ ID NOS: 12
;   SOFTWARE: PatentIn version 3.2

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Qy   4691 GAGCACAGCTGCGCAAGGAAGCGCCCGTGCTGGCCAGCCACGATAGCGCGCTGCCTCGTC 4750
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Db   4193 GAGCACAGCTGCGCAAGGAAGCGCCCGTGCTGGCCAGCCACGATAGCGCGCTGCCTCGTC 4134

Qy   4751 CTGCAGTTCATTCAGGGCACCGGACAGGTCGTCTTGACAAAAGAACCGGCGCCCCCCTG 4810
          |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db   4133 TTGCAGTTCATTCAGGGCACCGGACAGGTCGTCTTGACAAAAGAACCGGCGCCCCCCTG 4074

Qy   4811 CGCTGACAGCCGGAACACGGGCGCATCAGACGCAGCAGCCGATTGTCGTTGTGCCAGTCATA 4870
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4073 CGCTGACAGCCGGAACACGGGCGCATCAGACGCAGCAGCCGATTGTCGTTGTGCCAGTCATA 4014

Qy   4871 GCCGAATAGCCTTCCACCCAAGCGGCCGGAGGACTGCGTGCAATCCATCTTGTTCAAT 4930
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Db   4013 GCCGAATAGCCTTCCACCCAAGCGGCCGGAGGAACTGCGTGCAATCCATCTTGTTCAAT 3954

Qy   4931 CATGCGAAAAGATCCTCATCCTGTCCTTGATCAGATCTTGATCAGAGCTTGATCCCCTGCGCCATCAGAT 4990
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Db   3953 CATGCGAAAACATCCTCATCCTGTCTCTTGATCAGAGCTTGATCAGAGCTTGATCCCCTGCGCCATCAGAT 3894

Qy   4991 CCTTGGCGCGAAGAAAGCCATCCAGTTTACTTTGCAGGGCTTCCAACCTTACCAGAGGG 5050
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3893 CCTTGGCGCGAGAAAGCCATCCAGTTTACTTTGCAGGGCTTCCAACCTTACCAGAGGG 3834

Qy   5051 CGCCCCAGCTGCAATTCCGGTTCGCTTGCTGTCTGTCCATAAAACCGCCCAGTCTAGCTATCG 5110
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Db   3833 CGCCCCAGCTGCAATTCCGGTTCGCTTGCTGTCTGTCCATAAAACCGCCCAGTCTAGCTATCG 3774

Qy   5111 CCATGTAAGCCACTGCAAGCTACCTGCTTCTCTTGCGCTTGCGTTTCCCTTGTCCA 5170
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3773 CCATGTAAGCCACTGCAAGCTACCTGCTTCTCTTTGCGCTTGCGTTTCCCTTGTCCA 3714

Qy   5171 GATAGCCCAGTAGCTGACATTCATCCGGGGTCAGCACCGTTTCTGCGGCGACTGGCTTTCTA 5230
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3713 GATAGCCCAGTAGCTGACATTCATCCGGGGTCAGCACCGTTTCTGCGGCGACTGGCTTTCTA 3654

Qy   5231 CGTG 5234
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Db   3653 CGTG 3650
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RESULT 13
US-10-811-136B-10/c
; Sequence 10, Application US/10811136B
; Publication No. US20040025345A1
; GENERAL INFORMATION:
;   APPLICANT: AviGenics, Inc
;   TITLE OF INVENTION: Production of a Transgenic Avian by Cytoplasmic Injection
;   FILE REFERENCE: AVI-025CIPPCT
;   CURRENT APPLICATION NUMBER: US/10/811,136B
;   CURRENT FILING DATE: 2004-03-26
;   NUMBER OF SEQ ID NOS: 13
;   SOFTWARE: PatentIn version 3.2
;
; SEQ ID NO 10
;   LENGTH: 6233
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Plasmid pCR-XL-TOPO-CMV-pur-attB
US-10-811-136B-10

Query Match   30.9%;   Score 1634.4;   DB 20;   Length 6233;
Best Local Similarity 80.6%;   Pred. No. 0;
Matches 2082;   Conservative 0;   Mismatches 211;   Indels 291;   Gaps 3;

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Qy   2942 CTTCCGCTTCCTCGCTCACTGACTCCGCTCGTCCGGCTCGTCGGCGCGGAGCGGTAT 3001
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Db   6233 CTTCCGCTTCCTCGCTCACTGACTCCGCTCGTCCGGCTCGTCGGCGCGGAGCGGTAT 6174

Qy   3002 CAGCTCACTCAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGA 3061
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   6173 CAGCTCACTCAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGA 6114
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Qy   3803 AAGCGGGCCATCGTGCTCCCCACTCTCTGCGAGTTCGGGGGCATGGATGCGCGGATAGCCGC 3862
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Db   5273 GGGCGAACTCCCGCCCCACGGCTGCTGCGCGATCTCGGTCGCGATCGCCGGGCCGGAGGCGT 5214

Qy   3863 TGCTGGTTTCCTGGATGCCGACGACGGATTTGCACTGCCGGTAGAACTCCGCGAGGTCGTCCA 3922
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Db   5213 CCCGGAAGTTCGTGACACGACGACCTCCGACCACTCGGCGTACAGCTCGTCAGGCCGCGCA 5154

Qy   3923 GCC------- 3925
          |||
Db   3925 GCC------- 

Qy   5153 CCCACACCCAGGCCACGGGGTGTTCTCGGCGACCACCTGGTCCTGGACACCGGCTGATGAACA 5094
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Db   5094 CCCACACCCAGGCCACGGGGTGTTCTCGGCGACCACCTGGTCCTGGACACCGGCTGATGAACA

Qy   3926 ---TCAGGCAGCTGAACCAACTCGGCGGGGATCGAGGGGCCCGGGGTGGGCGAAGAACT 3982
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5093 GGGTCACGTCGTCCCGGACCACCACCGGCGGGAGTCGTCCTCCACGAAGTCGGGGGAACC 5034

Qy   3983 CCAGCATGAGATCCCCGCGGTGGAGGATCGATCAGCCGGCGTCCCGGCGTCCCGGAAAAACGATTCCGA 4042
          |||||||||||||||||||||| |||||
Db   5033 CGAGCCGGTGGTCCGGTCCAGAACTCGACCGCGGTCCGCGTGCGGTGCAGCACCGGA 4974

Qy   4043 AGCCCAACCTTTCATAGAAGGCGGCGGTGGAATCGAAATCTCGTGATGGCAGGTTGGGCG 4102
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4973 CGAGCCGGTGGTCCGGTCCAGAACTCGACCGCGGTCCGCGTGCGGTGCAGCACCGGA 4914

Qy   4103 TCGCTTGGTCGGTCATTTCGAACCCCAGAGTCCCG------- 4137
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Db   4913 CGGCACTGGTCAACTTGGTCCATGGTCGGCCCTCCTCACGGTGGCTATTATTGGAGCATTTATC 4854

Qy   4138 AGGGTTATTGTCTCATGAGCGGGATACATATTTGAATGTATTTTAGAAAAAAAATAAACAAATAG 4137
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Db   4137 

Qy   4853 GGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGTGATGCGGTGTGAAAATACCGCACAG 4794
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Db   4138 ---------CTCAGAGAACTC 

Qy   4793 ATGCGTAAGGAGAAAATACCGCATCAGGAAATTGTAAGCGTTAATATAATTCAGAAGAGAACTC 4734
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Db   4151 GTCAAGAAGCGCGATAGAAGGCGATGCGCTGCGAATCGGGAGCGGCGGATACCGTAAAGCAC 4210
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Db   4733 GTCAAGAAGCGCGATAGAAGGCGATGCGCTGCGAATCGGGAGCGGCGGATACCGTAAAGCAC 4674

Qy   4211 GAGGAAGCGGTCAGCCCATTCGCCGCCAAGCTCTTCAGCAATATCACGGGTAGCCAACGC 4270
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Db   4673 GAGGAAGCGGTCAGCCCATTCGCCGCCAAGCTCTTCAGCAATATCACGGGTAGCCAACGC 4614

Qy   4271 TATGTCCTGATAGCGGTCCGCGCACACCAGCGCCGGCCACACCCCAGCGTCGATGAATCCAGAAAAGCG 4330
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Db   4613 TATGTCCTGATAGCGGTCCGCGCACACCAGCGCCGGCCACACCCCAGCGTCGATGAATCCAGAAAAGCG 4554

Qy   4331 GCCATTTTCCACCATGATATTCGGCAAGCAGGCATCGCCATGGGTCACGACGAGATCCTC 4390
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Db   4553 GCCATTTTCCACCATGATATTCGGCAAGCAGGCATCGCCATGGGTCACGACGAGATCCTC 4494

Qy   4391 GCCGTCGGGCATGCGCGCCTTGAGCCTGGCCGAACAGTTCGGCTGGCGCGAGCCCCTGATG 4450
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Db   4493 GCCGTCGGGCATGCGCGCCTTGAGCCTGGCCGAACAGTTCGGCTGGCGCGAGCCCCTGATG 4434

Qy   4451 CTCTTCGTCCAGATCATCCTGATCGACAAGACCGGCTTCCATCCGAGTACGTGCTCGCTC 4510
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4433 CTCTTCGTCCAGATCATCCTGATCGACAAGACCGGCTTCCATCCGAGTACGTGCTCGCTC 4374

Qy   4511 GATGCGATGTTTCGCTTGGTCGTCGAATGGCAGTGCCGGATCAAGCGTATGCAGCCG 4570
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4373 GATGCGATGTTTCGCTTGGTCGTCGAATGGCAGTGCCGGATCAAGCGTATGCAGCCG 4314

Qy   4571 CCGCATTGCATCAGCCATGATGGATACTTTCTCGGCAGGAGCAAGGTGAGATGACAGGAG 4630
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4313 CCGCATTGCATCAGCCATGATGGATACTTTCTCGGCAGGAGCAAGGTGAGATGACAGGAG 4254

Qy   4631 ATCCTGCCCCGGCACTTCGCCCAATAGCAGCCAGTCCCTTCCCGCTTCAGTGACAACGTC 4690
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4253 ATCCTGCCCCGGCACTTCGCCCAATAGCAGCCAGTCCCTTCCCGCTTCAGTGACAACGTC 4194
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This page contains a nucleotide sequence alignment (query "Qy" versus database "Db") with paired sequence rows and position numbers. The alignment data is presented in two columns of stacked Qy/Db sequence blocks with flanking coordinate numbers.

Db 3953 CATGCCGAAACGATCCTCATCCTGTCTCTTGATCAGAGCTTGATCCCCTGCGCCATCAGAT 3894
Db 5873 GCGGTGGCGCTTTCTCATAGCTCACGCTGTAGTAGTATCTCAGTTCGGTGTGGTCGTTCGCT 5814

Qy 4991 CCTTGGCGCGCAAGAAAGCCATCAGTTACTTGGCAGGGCTTCCAACCTTACCAGAGGG 5050
Qy 3362 CCAAGCTGGGCTGTGTGCACGAACCCCCGTTGCAGCCGACCGCGCCCTTATCCGGTA 3421

Db 3893 CCTTGGCGCGCGAGAAAGCCATCAGTTACTTGGCAGGGCTTCCAACCTTACCAGAGGG 3834
Db 5813 CCAAGCTGGGCTGTGTGCACGAACCCCCGTTGCAGCCGACCGCGCCCTTATCCGGTA 5754

Qy 5051 CGCCCCAGCTGGCAATTCCGGTTCGGTCGTGTCCATAAAACCGCCCAGTCTAGCTATCG 5110
Qy 3422 ACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTG 3481

Db 3833 CGCCCCAGCTGGCAATTCCGGTTCGGTCGTGTCCATAAAACCGCCCAGTCTAGCTATCG 3774
Db 5753 ACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTG 5694

Qy 5111 CCATGTAAGCCCACTGCAAGCTACCTGCTTCTCTTTGCGCTTGCGTTTTCCCTGTCCA 5170
Qy 3482 GTAACAGGATTAGCAGCAGGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGC 3541

Db 3773 CCATGTAAGCCCACTGCAAGCTACCTGCTTCTCTTTGCGCTTGCGTTTTCCCTGTCCA 3714
Db 5693 GTAACAGGATTAGCAGCAGGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGC 5634

Qy 5171 GATAGCCCAGTAGCTGACATTCATCCGGGGTCAGCACCGGGGTCAGCACCG 5230
Qy 3542 CTAACACGGCTACACTAGAAGAACAGTATTGGTATCGGCCTCGTGCTGCTAGCCAGTTA 3601

Db 3713 GATAGCCCAGTAGCTGACATTCATCCGGGGTCAGCACCGGGGTCAGCACCG 3654
Db 5633 CTAACACGGCTACACTAGAAGGACAGTATTGGTATCGGCCTCGTGCTGCTAGCCAGTTA 5574

Qy 5231 CGTG 5234
Qy 3602 CCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAACAAACACCGCTGGTAGCGGTG 3661

Db 3653 CGTG 3650
Db 5573 CCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAACAAACAACCGCTGGTAGCGGTG 5514

RESULT 14
US-10-940-315-10/c
; Sequence 10, Application US/10940315
; Publication No. US2005003418GA1
; GENERAL INFORMATION:
;   APPLICANT: AviGenics, Inc
;   TITLE OF INVENTION: Site Specific Nucleic Acid Integration
;   FILE REFERENCE: AVI-025CIP3
;   CURRENT APPLICATION NUMBER: US/10/940,315
;   CURRENT FILING DATE: 2004-09-14
;   NUMBER OF SEQ ID NOS: 13
;   SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
;   LENGTH: 6233
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Plasmid pCR-XL-TOPO-CMV-pur-attB
US-10-940-315-10

Qy 3662 GTTTTTTGTTTTGCAAGCAGCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTT 3721
Db 5513 GTTTTTTGTTTTGCAAGCAGCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTT 5454

Query Match   30.9%;   Score 1634.4;   DB 21;   Length 6233;
Best Local Similarity   80.6%;   Pred. No. 0;
Matches 2082;   Conservative 0;   Mismatches 211;   Indels 291;   Gaps 3;

Qy 3722 TGATCTTTTCTACGGGGTCTGACGCTCAGTGGAACGAAAACTCACGTTAAGGGATTTTGG 3781
Qy 2942 CTTCCGCTTCCTCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTAT 3001

Db 5453 TGATCTTTTCTACGGGGTCTGACGCTCAGTGGAACGAAAACTCACGTTAAGGGATTTTGG 5394
Db 6233 CTTCCGCTTCCTCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTAT 6174

Qy 3782 TCATGAGATTATC-- 3794
Qy 3002 CAGCTCACTCAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGA 3061

Db 5393 TCATGAGATTATCAAAAAGGATCTTCACCTAGATCCTTTAAATTAAAAATGAAGTTTTA 5334
Db 6173 CAGCTCACTCAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGA 6114

Qy 3795 --GTCGACCA 3802
Qy 3062 ACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGT 3121

Db 5333 GCACGTGTCAGTCTGCTCCTCGGCCACGAAGTGCACGCAGTTGCCGGATGCGGCGATAGCGGCA 5274
Db 6113 ACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGT 6054

Qy 3803 AAGCGGCCATCGGACTCCCACTCGTCCCCCACTCGTCAGTTGCGGGGGCATGATGCGGATAGCGCGC 3862
Qy 3122 TTTTCCATAGGCTCCGCCCCCCTGACGAGCATCACAAAATGACGCTCAAGTCAGAGGT 3181

Db 5273 GGGCGAACTCCCGCGTCTCGCCGATCTCGTCGCCGATCTCGTCTGCCGGTGACAACTCCGCGAGGTCGTCCA 5214
Db 6053 CGGCACTGGTCAACTTGGCCACGTGTGGCCCTTCCTCCACGTGTCGTCATTATCG 5994

Qy 3863 TGCTGGTTCCTGGATGCCGACGGATTTGCACTGCCCGGTAGAACTCCGGCGAGGTCGTCCA 3922
Qy 4103 TCGCTTGGTCGGTCATTTGAACCCCAGAGTCCCG------------------------ 4137

Db 5213 CCCGGGAAGTTCGTGGGACACGGACACCTTCGTCTCCAGCTCGTCCTCCAGGCCCGCGCA 5154
Db 4913 AGGGTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACAAATAG 4854

Qy 3923 GCC--- 3925
Qy 4138 --- 4137

Db 5153 CCCACACCAGGCCAGGGTGGTTGTCTCGGCACCACCTGGTCCTCGGACCGCGCTGATGAACA 5094
Db 4138 --- 4138

Qy 3926 ---TCAGGCAGCAGCTGAACCAACTCGGAGGGGGATCGAGCCCGGGGTGGGCGAAGAACT 3982
Qy 4853 GGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGTGAAATACCGCACAG 4794

Db 5093 GGGTCACGTCGTCCCGACCACACCGCGAAGTCGTCCTCCACGAAGTCGTCCCGGGAGAACC 5034
Db 5873 GGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGTGTGAAATACCGCACAG 5814

Qy 3983 CCAGCATGAGATCCCGCGCTGGAGGATCATCCAGCCGCGCTCCCGAAAACGATTCCGA 4042
Qy 3242 GCTCTTCCTCGTCCGACACTGAGCTCCGCTTACGACCTGCGTCCTTTCTCCCTTCTCGGAA 3301

Db 5033 CGAGCCGGTCGGTCGGTCCGACCGCTCGGAACTCGACAGTCGGTCGGTCGTGAGCACCGGAA 4974
Db 5933 GCTCTTCCTCGTCCGACACTGAGCTCCGCTTACGACCTGCGTCCTTTCTCCCTTCTCGGAA 5874

Qy 4043 AGCCCAACCTTTCATAGAAGGCGGCGGTGAATCGAAATCTCGATGCATTATCC 4102
Qy 3302 GCGGTGGCGCTTTCTCATAGCTCACGCTGTAGTATCTCAGTTCGGTGTGGTCGTTCGCT 3361

Db 4973 CGGCACTGGTCAACTTGGCCACGTGTGGCCCTTCCTCCACGTGTCGTCATTATTC 4914
Db 3361

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Qy        5231 CGTG 5234
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Db        3653 CGTG 3650
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RESULT 15
US-10-950-050-10/c
;  Sequence 10, Application US/10950050
;  Publication No. US2005006383A1
;  GENERAL INFORMATION:
;     APPLICANT: AviGenics, Inc
;     TITLE OF INVENTION: Site Specific Recombination in Avians
;     FILE REFERENCE: AVI-025CON
;     CURRENT APPLICATION NUMBER: US/10/950,050
;     CURRENT FILING DATE:  2004-09-24
;     NUMBER OF SEQ ID NOS: 12
;     SOFTWARE: PatentIn version 3.2
;  SEQ ID NO 10
;     LENGTH: 6233
;     TYPE: DNA
;     ORGANISM: Plasmid pCR-XL-TOPO-CMV-pur-attB
US-10-950-050-10

Query Match       30.9%;  Score 1634.4;  DB 21;  Length 6233;
Best Local Similarity   80.6%;  Pred. No. 0;
Matches 2082;  Conservative   0;  Mismatches   211;  Indels   291;  Gaps   3;
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Qy        2942 CTTCCGCTTCCTCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTAT 3001
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        6233 CTTCCGCTTCCTCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTAT 6174

Qy        3002 CAGCTCACTCAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGA 3061
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        6173 CAGCTCACTCAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGA 6114

Qy        3062 ACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGT 3121
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        6113 ACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGT 6054

Qy        3122 TTTTCCATAGGCTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGT 3181
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        6053 TTTTCCATAGGCTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGT 5994

Qy        3182 GGCGAAACCCGACAGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGC 3241
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Db        5993 GGCGAAACCCGACAGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGC 5934

Qy        3242 GCTCTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAA 3301
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Db        5933 GCTCTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAA 5874

Qy        3302 GCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCT 3361
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Db        5873 GCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCT 5814

Qy        3362 CCAAGCTGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTA 3421
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Db        5813 CCAAGCTGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTA 5754

Qy        3422 ACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTG 3481
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Db        5753 ACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTG 5694

Qy        3482 GTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGC 3541
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Db        5693 GTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGC 5634

Qy        3542 CTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTA 3601
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Db        5633 CTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTA 5574

Qy        3602 CCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAACCACCGCTGGTAGCGGTG 3661
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Qy        4151 GTCAAGAAGGCGATAGAAGGCGATGCGCTGCGAATCGGGAGCGGCGATACCGTAAAGCAC 4210
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Qy        4211 GAGGAAGCGGTCAGCCCATTCGCCGCCAAGCTCTTCAGCAATATCACGGGTAGCCAACGC 4270
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Qy        4271 TATGTCCTGATAGCGGTCCGCCACACCCAGCCGGCCACAGTCGATGAATCCAGAAAAGCG 4330
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Qy        4331 GCCATTTTCCACCATGATATTCGGCAAGCAGGCATCGCCATGGGTCACGACGAGATCCTC 4390
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Qy        4391 GCCGTCGGGCATGCGCGCCTTGAGCCTGGCGAACAGTTCGGCTGGCGCGAGCCCCTGATG 4450
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Qy        4451 CTCTTCGTCCAGATCATCCTGATCGACAAGACCGGCTTCCATCCGAGTACGTGCTCGCTC 4510
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Qy        4511 GATGCGATGTTTCGCTTGGTGGTCGAATGGGCAGGTAGCCGGATCAAGCGTATGCAGCCG 4570
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Qy        4571 CCGCATTGCATCAGCCATGATGGATACTTTCTCGGCAGGAGCAAGGTGAGATGACAGGAG 4630
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Db        4313 CCGCATTGCATCAGCCATGATGGATACTTTCTCGGCAGGAGCAAGGTGAGATGACAGGAG 4254

Qy        4631 ATCCTGCCCCGGCACTTCGCCCAATAGCAGCCAGTCCCTTCCCGCTTCAGTGACAACGTC 4690
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Qy        4751 CTGCAGTTCATTCAGGGCACCGGACAGGTCGGTCGGTCTTGACAAAAAGAACCGGGCCCTG 4810
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Qy   5231 CGTG 5234
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Db   3653 CGTG 3650

Search completed: July 3, 2005, 07:52:29
Job time : 2975 secs

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Qy   3722 TGATCTTTTCTACGGGTCTGACGCTCAGTGGAACGAAAACTCACGTTAAGGGATTTTGG 3781
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Qy   3782 TCATCAGATTATC---- 3794
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Qy   3795 ------------------GTCGACCA 3802
Db   5333 GCACGTGTCAGTCCTGCTCCGGCCACGAAGTGCACGCAGTTGCCGCGGGTGCGCGCA 5274

Qy   3803 AAGCCGGCCATCGTGCTCCCCCACTCGCAGTTCGGGGGCATGGCGCGGGATAGCCGC 3862
Db   5273 GGGCGAACTCCCGCCCCCACGGCTGCTCGGCCGATCTCGGTCATGGCCCGGAGGGCGT 5214

Qy   3863 TGCTCGGTTTCCTGGATGCCGACGGATTTGCACTGCCGGTAGAACTCCGCCAGTCGTCCA 3922
Db   5213 CCCGGAAGTTCGTGGACACGACCTCCGGACCACTCCGGCGTACAGCTCGTCGTCCAGGCCGCGCA 5154

Qy   3923 GCC---------------- 3925
Db   5153 CCCACACCCCAGGCCAGGGTGTTGTCCGGCCACCACCTGGTCCTGGACACGGCGCGCTGATGAACA 5094

Qy   3926 ---TCAGGCAGCAGTGAACCAACTCGGCAGGGGATCGGCGAGCCGGGTGGGCGGAAGAACT 3982
Db   5093 GGGTCACGTCGTCCCGGACCACACCGGAAGTCGTCCTCCACGAAGTCCCGGAGGAACC 5034

Qy   3983 CCAGCATGAGAGATCCCCGGCTGGAGGATCATCCAGCCGGCGTCCCGGAAAACGATTCCGA 4042
Db   5033 CGAGCCGGCGTCGGTCCAGAACTCGGACCGGCGACGTCGCGCGGCCGGTGAGCACCGGAA 4974

Qy   4043 AGCCCAACCTTTCATAGAAGGCGGCGGTGGAATCGAAATCGTGATGGCAGGTTGGGCG 4102
Db   4973 CGGCACTGGTCAACTTGGCCATGGTGGCCCTCCTCACGTGCTATTATTGAAGCATTTATC 4914

Qy   4103 TCGCTTGGTCGGTCATTTCGAACCCCAGCTCCCG- 4137
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Db   4853 GGGTTCCGCGCACATTCCCGAAAAGTGCCACCTGTATGCGGTGTGAAATACCGCACAG 4794

Qy   4138 ----------------CTCAGAAGAACTC 4150
Db   4793 ATGGCGTAAGGAGAGAAAATACCCGATCCAGGAAATTGTAAGCGTTAATAATTCAGAAGAACTC 4734

Qy   4151 GTCAAGAAGGCGATAGAAGGCGATGCGCTGCGAATCGGCAGCGGCGATACCGTAAAGCAC 4210
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Db   4613 TATGTCCTGATAGCGGTCCGCCACACCAGCCGGCCACAGTCGATGAATCCAGAAAAGCG 4554

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Qy   4391 GCCGTCGGGCATGCGCGCCTTGAGCCTGGCGAACAGTTCGGCTGGCGCGAGCCCCTGATG 4450
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Db   4493 GCCGTCGGGCATGCGCGCCTTGAGCCTGGCGAACAGTTCGGCTGGCGCGAGCCCCTGATG 4434

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 3, 2005, 06:18:19 ; Search time 15530 Seconds
                                    (without alignments)
                                    12948.714 Million cell updates/sec

Title: US-09-921-143-36
Perfect score: 5283
Sequence: 1 aagcttgacctatgcgact.........tgagtgcttgcggcagcgtg 5283

Scoring table: IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   EST:*
              1: gb_est1:*
              2: gb_est2:*
              3: gb_htc:*
              4: gb_est3:*
              5: gb_est4:*
              6: gb_est6:*
              7: gb_est5:*
              8: gb_gss1:*
              9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Match	Query Length	DB	ID	Description
	1	991	18.8	2450	3	AK047844	AK047844 Mus muscu
	2	948	17.9	1067	7	AU081137	AU081137
c	3	939.4	17.8	954	7	CK283361	CK283361 EST746083
c	4	924.6	17.5	947	7	CK298208	CK298208 EST760922
	5	919.3	17.4	1089	7	AU081124	AU081124 AU081124
	6	918.6	17.4	935	7	CK284786	CK284786 EST747508
c	7	911	17.2	936	7	CK256977	CK256977 EST740614
c	8	907	17.2	910	7	CK287930	CK287930 EST750652
c	9	897.4	17.0	1049	9	CL021189	CL021189 CH216-8A1
	10	886.4	16.8	933	7	CK291799	CK291799 EST754513
c	11	875	16.6	925	6	CB686151	CB686151 Bn01b_02o
	12	866.2	16.4	1073	7	CF269652	CF269652 Fcylcold8
	13	859.2	16.3	885	9	CL076016	CL076016 CH216-138
c	14	843	16.0	856	7	CK287297	CK287297 EST750019
	15	820.6	15.5	1025	9	CL021193	CL021193 CH216-8A1
	16	818.6	15.5	1169	9	AG332951	AG332951 Mus muscu
	17	809.2	15.3	966	8	BZ570738	BZ570738 msh2_1513
	18	805.8	15.3	865	7	CK125894	CK125894 BES182411
c	19	803	15.2	804	7	CK291519	CK291519 EST754233
c	20	794	15.0	811	7	CK288185	CK288185 EST750907
c	21	781.4	14.8	846	7	CV468077	CV468077 est_1_van
	22	781.2	14.8	1163	4	AU081044	AU081044 AU081044
	23	781.2	14.8	1249	8	BZ572284	BZ572284 msh2_2572
	24	780.8	14.8	831	4	BG680919	BG680919 602628716
c	25	780.8	14.8	858	6	CA488579	CA488579 AGENCOURT
	26	780.6	14.8	833	6	CB686421	CB686421 Bn01b_04j
	27	774	14.7	954	1	AL044364	AL044364 DKFZp434C
	28	769.2	14.6	863	7	CF752100	CF752100 TGDR9_Hum
c	29	760.8	14.4	878	7	CK288711	CK288711 EST751433
	30	754	14.3	1369	8	BZ579291	BZ579291 msh2_6285
	31	752	14.2	752	6	CD646006	CD646006 SSPG526R
	32	746.2	14.1	778	5	BP539067	BP539067 BP539067
	33	746	14.1	844	8	BZ574513	BZ574513 msh2_3706
	34	742.2	14.0	1346	8	BZ572730	BZ572730 msh2_2771
	35	740.8	14.0	914	8	BZ569398	BZ569398 pacs2-164
	36	740.4	14.0	831	9	TBR548748	TBR548748 Trypanoso
	37	740	14.0	1194	8	BZ578985	BZ578985 msh2_6095
	38	735.4	13.9	907	5	BP539126	BP539126 BP539126
c	39	734.8	13.9	811	9	AJ517156	AJ517156 Arabidops
	40	730	13.8	756	7	CO477685	CO477685 GQ0132.B7
	41	726	13.7	793	7	CK122681	CK122681 BES182410
	42	725.6	13.7	959	8	BZ557985	BZ557985 pacs1-60
	43	724.6	13.7	2333	3	CR701632	CR701632 Tetraodon
	44	719.6	13.6	847	8	AZ687169	AZ687169 ENTMP05TF
	45	719.6	13.6	854	8	BZ570648	BZ570648 msh2_1469

ALIGNMENTS

RESULT 1
AK047844
LOCUS   AK047844   2450 bp   mRNA   linear   HTC 03-APR-2004
DEFINITION Mus musculus 16 days embryo head cDNA, RIKEN full-length enriched
            library, clone:C130004M09 product:vascular endothelial growth
            factor C, full insert sequence.
ACCESSION   AK047844
VERSION   AK047844.1 GI:26339001
KEYWORDS   HTC; CAP trapper.
SOURCE   Mus musculus (house mouse)
ORGANISM   Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
AUTHORS   Carninci,P. and Hayashizaki,Y.
TITLE   High-efficiency full-length cDNA cloning
JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
MEDLINE   99279253
PUBMED   10349636
REFERENCE   2
AUTHORS   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE   Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL   Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE   20499374
PUBMED   11042159
REFERENCE   3
AUTHORS   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
            Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
            Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
            Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
            Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
            Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
            Okazaki,Y., Muramatsu,M., Inoue,K., Kira,A. and Hayashizaki,Y.
TITLE   RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer
JOURNAL   Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE   20530913
PUBMED   11076861
REFERENCE   4
AUTHORS   The RIKEN Genome Exploration Research Group Phase II Team and the
            FANTOM Consortium.
TITLE   Functional annotation of a full-length mouse cDNA collection.
JOURNAL   Nature 409, 685-690 (2001)
REFERENCE   5
AUTHORS   The FANTOM Consortium and the RIKEN Genome Exploration Research

TITLE   Group Phase I & II Team.
            Analysis of the mouse transcriptome based on functional annotation
            of 60,770 full-length cDNAs
JOURNAL   Nature 420, 563-573 (2002)
REFERENCE   6 (bases 1 to 2450)
AUTHORS   Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,
            Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,
            Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T.,
            Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T.,
            Katoh,H., Kawai,J., Kojima,Y., Konno,S., Konno,H., Kouda,M.,
            Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M.,
            Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N.,
            Okazaki,Y., Saito,H., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N.,
            Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
            Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,
            Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
            Muramatsu,M. and Hayashizaki,Y.
TITLE   Direct Submission
JOURNAL   Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
            Physical and Chemical Research (RIKEN), Laboratory for Genome
            Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
            RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
            Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp,
            URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
            Fax:81-45-503-9216)
COMMENT   cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues.
            Please visit our web site for further details.
            URL:http://genome.gsc.riken.jp/
            URL:http://fantom.gsc.riken.jp/.
FEATURES   Location/Qualifiers
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                     /mol_type="mRNA"
                     /strain="C57BL/6J"
                     /db_xref="FANTOM DB:C130004M09"
                     /db_xref="taxon:10090"
                     /clone="C130004M09"
                     /tissue_type="head"
                     /clone_lib="RIKEN full-length enriched mouse cDNA library"
                     /dev_stage="16 days embryo"
     CDS   175..1422
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                     vascular endothelial growth factor C (MGD|MGI:109124,
                     GB|NM_009506, evidence: BLASTN, 99%, match=1784)"
                     /codon_start=1
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                     /db_xref="GI:26339002"
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                     GGEVKAFEFGKDLEEQLRSVSSVDELMSVLYPDYWKMYKCQLRKGGWQQPTLNTRTGDS
                     VKFAAAHYNTEILKSIDNEWRKTQCMPREVCIDVGKEFGAATNTFFKPPCVSVSYRCGG
                     CCNSEGLQCMNTSTGYLSKTLFEITVPLSQGPKPVTISFANHTSRCMSKLDVYRQVH
                     SIIRRSLPATLPQCQAANKTCPTNYVWNNYMCRCLAQQDFIFYSNVEDDSTNGFHDVC
                     GPNKELDEDTCQCVCKGGLRPSSCGPHKELDRDSCQCVCKNKLFPNSCGANREFDENT
                     CQCVCKRTCPRNQPLNPGKCACSCTENTQKCFLKGKKFHHQTCSCYRRPCANRLKHCD
                     PGLSFSEEVCRCVPSYWKRPHLN"
ORIGIN

Query Match   18.8%; Score 991; DB 3; Length 2450;
Best Local Similarity 85.4%; Pred. No. 1.3e-273;
Matches 1121; Conservative   0; Mismatches 180; Indels 12; Gaps   1;

Qy   481 CACCTGGGTTGGGATCGATCCATCATGCACTCGCTGGGCTTCTTCTCGTGGGCTGTTCT 540
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Db   151 CTCCCTGCTTCCCGGTCCATCCACCATGCACTTGCTGTGCTTCTTGTCTCTGGCGTGTCC 210

Qy   541 CTGCTCGCCGCGCTGCTCCCGGTCCCGGTTCTCCGCGAGGCGCGCGCCGCGCTCC 600
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Db   211 CTGCTCGCCGCGCTGCTGGCTGATCCCCAGTCCCGAGCGCCCGCGGCGCACCGTGCCGCCCTTC 270

601 GAGTCGGACTCGACCTCTCGGACGCGGACCGGGAGCCCGACGCGGGTGAGGCCACGGCTTATGCA 660
    |||||||||||||| |||||||||||| ||||| |||| ||||| ||||||||||||||||||
271 GAGTCGGGACTGGGCTTCTCGGAAGCCGAGCCCGACGGGGGCGAGTCAAGGCTTTTGAA 330

661 AGCAAGATCTGGAGGAGCAGTACGGTCTCGTGTCCAGTGTAGATGAACTCATGACTGTA 720
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331 GGCAAAGACCTGGAGGAGCAGTGCGGTCTGTGTCGTGTCCAGTGTAGATGAGTGATGTGTC 390

721 CTCTACCCAGATATTGGAAAATGTACAAGTGTCAGCTAAGGAAAGGAGGCTGGCAACAT 780
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391 CTGTACCCAGACTACTGGAAAATGTACAAGTGCCAGCTGCGCAAAGGCGGGCTGGC----- 445

781 AACAGAGAACAGGCCCAACCTCAACTCAAGGACAGCAGAGAGACTATAAAATTGCTGCAGCA 840
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446 ------AGCAGCCACCCTCAATACCAGGACACAGGGGACAGTGTAAAATTGCTGCTGCA 498

841 CATTATAATACAGAGATCTTGAAAAGTATTGATAATGAGTGGAGAAAAGACTCAATGCATG 900
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499 CATTATAACACAGAGATCCTGAAAAGTATTGATAATGAGTGGAGAAGAGACTCAATGCATG 558

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559 CCACGTGAGGTGTGTATAGATGTGGGGAAGGAGTTTGGAGCAGCCCAAAACACCTTCTTT 618

961 AAACCTCCATGTGTGTCCGTCTACAGATGTGGGGGTGCTGCAATAGTGAGGGGCTGCAG 1020
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619 AAACCTCCATGTGTGTCCGTCTACAGATGTGGGGGTGCTGCAACAGCGAGGGGCTGCAG 678

1021 TGCATGAACACCAGCACGAGCTACCTTCAGCAAGACGTATTTATTGAAATTACAGTGCCTCTC 1080
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679 TGCATGAACACCAGCACCAGGTACCTCAGCAAGACGTTGTTTGAAATTACAGTGCCTCTC 738

1081 TCTCAAGGCCCCAAACCAGTAACAATCAGTTTGCCAATCAGTTTGCCGATGCGATGCATG 1140
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739 TCACAAGGCCCCAAACCAGTCACAATCAGTTTGCCAATCAGTTTGCCGGTGCGATGCATG 798

1141 TCTAAACTGATGTTTACAGACAAGTTCATTCCATTATTAGACGTTCCTGCCAGCAACA 1200
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799 TCTAAACTGACGAGTGATGTTTACAGACAAGTTCATTCATTATTAGACGTTCTCTGCCAGCAACA 858

1201 CTACCACAGTGTCAGGCAGCGAACAAGACCTGCCCACCAATTACATGTGGAATAATCAC 1260
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859 TTACCACAGTGTCAGGCAGCGAACAAGACATGTCCAACAAACTATGTGTGGAATAACTAC 918

1261 ATCTGCAGATGCCTGGCTCAGGAGGAGATTTTATGTTTCCTCGGATGCGTGGAGATGACTCA 1320
     |||||| |||||||| |||||||||| |||| ||||||||||||| |||||||||||||
919 ATGTGCCGATGCCTGGCTCAGCAGGAGATTTTTATCTTTTATTCAAATGTGAAGATGACTCA 978

1321 ACAGATGGATTCCATGACATCTGTGACCAAACAAGGAGGCTGGATGAAGAGACCTGTCAG 1380
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979 ACCAATGGATTCCATGATGTCTGTGGACCCCCAACAAGGAGTGGATGAAGAAGACACCTGTCAG 1038

1381 TGTGTCTGCAGAGCGGCTTCGGCCTGCCTGCCAGCTGTGGACCCCCAGCAATGTGGGCCAACCGA 1440
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1039 TGTGTCTGCAAGGGGGGGCCTTGCAGGCCATCATCAGTTGTGGACCCCACCCAGCAACTAGATAGA 1098

1441 AACTCAGTGTCTGTAAAACAACATGCCAGTGTATGTAAAGACCTCTTCCCAGCAATGTGGGCCAACCGA 1500
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1099 GACTCAGTGTCAGTGTCTGTAAAAACAACAAACTTTTCCTAATTCATTGTGGAGGCAACAGG 1158

1501 GAATTTGATGAAACAAACATGCCAGTTGTATGTATGAAGAACCTGCCCCAGAAATCAACCC 1560
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1159 GAATTTGATGAGAATCAACATGTTCAGTGTGTATGTATGAAGAAACAGTGTCCAAGAAATCAGCCC 1218

1561 CTAAATCCTGGAAAATGTGCCTGTGAAATGTCCACAGAAGTCCACACAGAAATGCTTGTTAAAA 1620
     |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
1219 CTGAATCCTGGGAAATGTGCCTGTGAAATGTCGTGTGAAATGACACACAGAAAACACACAGAAGTGCTTCCTTAAA 1278

1621 GGAAAGAAGTTCCACCACACCAAAATGTTCCATCGAGCCATTGACAAACGAGCCGCCAG 1680
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1279 GGGAAGAAGTTCCACCATCAACATGCAGTTGTTACAGAAGACCGTGTGCGAATCGACTG 1338

1681 AAGGCTTGTGAGCCAGGATTTTCATATAGTGAAGAAGTGTGTCGTTGTGTCCCTTCATAT 1740

Db 1339 AAGCATTGTGATCCAGAGACTGTCCTTTAGTGAAGAGTATGCCGCTGTGTGTCCATCGTAT 1398
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Qy 1741 TGGAAAAGACCACCAAATGAGCTAATCTAGGATCCGTACCCTGCCCAGGCTTT 1793
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Db 1399 TGGAAAAGGCCCACATCTGAACTAAGACATCATACCCAGTTTTCAGTCCACCATTTT 1451

RESULT 2
AU081137
LOCUS   AU081137   1067 bp   mRNA   linear   EST 30-JUL-2002
DEFINITION   AU081137 Oncorhynchus mykiss Kidney infected by infectious
             hematopoietic necrosis virus Oncorhynchus mykiss cDNA clone KI2,
             mRNA sequence.
ACCESSION   AU081137
VERSION   AU081137.1 GI:6431485
KEYWORDS   EST.
SOURCE   Oncorhynchus mykiss (rainbow trout)
ORGANISM   Oncorhynchus mykiss
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Actinopterygii; Neopterygii; Teleostei; Euteleostei;
             Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
REFERENCE   1 (bases 1 to 1067)
AUTHORS   Kono,T., Sakai,M. and LaPatra,S.E.
TITLE   Expressed Sequence Tag Analysis of Kidney and Gill Tissues from
             Rainbow Trout (Oncorhynchus mykiss) Infected with Infectious
             Hematopoietic Necrosis Virus
JOURNAL   Mar. Biotechnol. 2 (5), 493-498 (2001)
COMMENT   Contact: Masahiro Sakai
             Faculty of Agriculture
             Miyazaki University
             1-1 nishi gakuenkibanadai, Miyazaki, Miyazaki 889-2192, Japan
             Email: m.sakai@cc.miyazaki-u.ac.jp.
FEATURES   Location/Qualifiers
     source   1..1067
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                     /db_xref="taxon:8022"
                     /clone="KI2"
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                     /clone_lib="Oncorhynchus mykiss Kidney infected by
                     infectious hematopoietic necrosis virus"
                     /note="common name:rainbow trout ; infected by infectious
                     hematopoietic necrosis virus"
ORIGIN

Query Match   17.9%; Score 948; DB 1; Length 1067;
Best Local Similarity 98.8%; Pred. No. 2.5e-261;
Matches 976; Conservative 0; Mismatches 10; Indels 2; Gaps 2;

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Db   82 CTTGGCGTAATCATGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCC 141

Qy 2766 ACACAACATACGAGCCCGGAAGCATAAAGTGTAAAGCCTGGGTGCCTAATCAGTGAGCTA 2825
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Db 142 ACACAACATACGAGCCCGGAAGCATAAAGTGTAAAGCCTGGGTGCCTAATCAGTGAGCTA 201

Qy 2826 ACTCACATTAATTGCGTTGCCCTACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCA 2885
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 202 ACTCACATTAATTGCGTTGCCCTACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCA 261

Qy 2886 GCTGCATTAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTC 2945
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 262 GCTGCATTAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTC 321

Qy 2946 CGCTTCCTCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGC 3005
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 322 CGCTTCCTCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGC 381

Qy 3006 TCACTCAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACAT 3065
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 382 TCACTCAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACAT 441

Qy 3066 GTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTT 3125
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Db 442 GTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTVTT 501

Qy 3126 CCATAGGCTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCG 3185
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Db 502 CCATAGGCTCCGCCCCCCTGACGAGCATCACAAAATCGACGCTCAAGTCAGAGGTGGCG 561

Qy 3186 AAACCCGACAGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTC 3245
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Db 562 AAACCCGACAGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTC 621

Qy 3246 TCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGT 3305
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Db 622 TCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGT 681

Qy 3306 GGGGCTTTCTCATAGCTCACGCTGTAGTATCTCAGTTCGGTGTGAGGTCGTTCGCTCCAA 3365
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Db 682 GGCGCTTTCTCATAGCTCACGCTGTAGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAA 741

Qy 3366 GCTGGGCTGTGTGCACGAACCCCCGTTCAGCCGACCGCTGCGCCTTATCCGGTAACTA 3425
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Db 742 GCTGGGCTGTGTGCACGAACCCCCGTTCAGCCGACCGCTGCGCCTTATCCGGTAACTA 801

Qy 3426 TCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAA 3485
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Db 802 TCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAA 861

Qy 3486 CAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAA 3545
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Db 862 CAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAA 921

Qy 3546 CTACGGCTACACTAGAAGAACAGTATTTGGTATCGGCCTCTGCGCTCTGCTGAAGCCAGTTACCTT 3605
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 922 CTACGGCTACACTAGAAGGACAGTATTTGGTATCGGCCTCTGCGCTCTGCTGAAGCCAGTTACCTT 981

Qy 3606 CGGAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTT 3665
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Db 982 CGGAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAA-CAACGCGTCGTAGCGCGTGTTTTT 1040

Qy 3666 TTTTGTTTGCAAGCAGCAGATTACGCGC 3693
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Db 1041 TTTTGTTTGC-AGCAGCAGATTACGCGC 1067

RESULT 3
CK283361/c
LOCUS   CK283361/c   Length 1067;
DEFINITION   EST746083 Nicotiana benthamiana mixed tissue cDNA library,
             normalized, full-length Nicotiana benthamiana cDNA clone NBMAG50 5'
             end, mRNA sequence.
ACCESSION   CK283361
VERSION   CK283361.1 GI:39855898
KEYWORDS   EST.
SOURCE   Nicotiana benthamiana
ORGANISM   Nicotiana benthamiana
             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
             Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
             asterids; lamiids; Solanales; Solanaceae; Nicotiana.
REFERENCE   1 (bases 1 to 954)
AUTHORS   Buell,C.R., Hart,A., Zismann,V., Karamycheva,S.A., Day,B.,
             Staskawicz,B., Jin,H. and Baker,B
TITLE   Generation of EST sequences from Nicotiana benthamiana
JOURNAL   Unpublished (2003)
COMMENT   Other_ESTs: EST746084
             Contact: Robin Buell
             The Institute for Genomic Research
             9712 Medical Center Dr, Rockville, MD 20850, USA
             Email: potato-array@tigr.org
             Clones can be requested from the University of Arizona Genomics
             Institute via http://genome.arizona.edu/orders/.
             Seq primer: ATT TAG GTG ACA CTA TAG.

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Db    294  CCAATAGCAGCCAGTCCCTTCCCGCTTCAGTGACAACGTTCGAGCACAGCAGCTGCGCAAGGAA  235
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Qy   4711  CGCCCGTCGTGGCCAGCCACGATAGCCGCGGCCTGCCTCGTCCTGCCAGTTCATTCAGGGCAC  4770
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    234  CGCCCGTCGTGGCCAGCCACGATAGCCGCGGCCTGCCTCGTCCTGCCAGTTCATTCAGGGCAC  175
           
Qy   4771  CGGACAGGTCGGTTCTTGACAAAAGAACAGGGCGCCCCCGCGTTGACAGCCGGAACACGG  4830
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    174  CGGACAGGTCGGTCTTGACAAAAGAACCGGGCGCCCCGCGTTGCGCTGACAGCCGGAACACGG  115
           
Qy   4831  CGGCATCAGAGCAGCAGCCGATTGTCGTTGTGCCAGTCATCAGCCGAATAGCCTCTCCACCC  4890
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    114  CGGCATCAGAGCAGCAGCCGATTGTCGTTGTGCCCAGTCATCAGCCGAATAGCCTCTCCACCC  55
           
Qy   4891  AAGCGGCCCGGAGAACCTGCGTGCAATCCATCTTGTTCAATC  4931
           ||||||||||||||||||||||||||||||||||||||||||
Db     54  AAGCGGCCCGGAGAACCTGCGTGCAATCCATCTTGTTCAATC  14
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RESULT 4

CK298208/c

LOCUS   CK298208   947 bp   mRNA   linear   EST 02-AUG-2004
DEFINITION   EST760922 Nicotiana benthamiana mixed tissue cDNA library,
             normalized, full-length Nicotiana benthamiana cDNA clone NBMDE30 5'
             end, mRNA sequence.
ACCESSION   CK298208
VERSION   CK298208.1 GI:39885354
KEYWORDS   EST.
SOURCE   Nicotiana benthamiana
  ORGANISM   Nicotiana benthamiana
             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
             Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
             asterids; lamiids; Solanales; Solanaceae; Nicotiana.
REFERENCE   1 (bases 1 to 947)
  AUTHORS   Buell,C.R., Hart,A., Zismann,V., Karamycheva,S.A., Day,B.,
             Staskawicz,B., Jin,H. and Baker,B.
  TITLE   Generation of EST sequences from Nicotiana benthamiana
  JOURNAL   Unpublished (2003)
COMMENT   Other_ESTs: EST760923
             Contact: Robin Buell
             The Institute for Genomic Research
             9712 Medical Center Dr, Rockville, MD 20850, USA
             Email: potato-array@tigr.org
             Clones can be requested from the University of Arizona Genomics
             Institute via http://genome.arizona.edu/orders/ .
             Seq primer: ATT TAG GTG ACA CTA TAG.
FEATURES   Location/Qualifiers
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                     /organism="Nicotiana benthamiana"
                     /mol_type="mRNA"
                     /db_xref="taxon:4100"
                     /clone="NBMDE30"
                     /tissue_type="abiotic and biotic stress-treated leaves,
                     callus tissue and root tissue"
                     /lab_host="DH10B-TonA"
                     /clone_lib="Nicotiana benthamiana mixed tissue cDNA
                     library, normalized, full-length"
                     /note="Vector: pCMVsport6.1; Site 1: EcoRI; Site 2: NotI;
                     supplier: RNA was isolated from Nicotiana benthamiana
                     tissues that include callus, roots from liquid culture
                     grown plants, heat-stressed leaves (38 C, 3 hr and 6 hr),
                     cold-stressed leaves (5 C 3 hr, 6hr), and pathogen
                     challenged leaves (Pseudomonas syringae pv tomato 12 hr;
                     Xanthomonas campestris pv campestris 12 hr, 18hr;
                     Pseudomonas syringae pv phaseolicola 18hr, and Xanthomonas
                     campestris pv vesicatoria 18hr). RNA was isolated from
                     these tissues and pooled in approximately equal molar
                     amounts."
ORIGIN

Query Match   17.5%;   Score 924.6; DB 7; Length 947;
Best Local Similarity 99.6%;   Pred. No. 1.4e-254;
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FEATURES             Location/Qualifiers
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                     /db_xref="taxon:4100"
                     /clone="NBMAG50"
                     /tissue_type="abiotic and biotic stress-treated leaves,
                     callus tissue and root tissue"
                     /lab_host="DH10B-TonA"
                     /clone_lib="Nicotiana benthamiana mixed tissue cDNA
                     library, normalized, full-length"
                     /note="Vector: pCMVsport6.1; Site 1: EcoRI; Site 2: NotI;
                     supplier: RNA was isolated from Nicotiana benthamiana
                     tissues that include callus, roots from liquid culture
                     grown plants, heat-stressed leaves (38 C, 3 hr and 6 hr),
                     cold-stressed leaves (5 C 3 hr, 6hr), and pathogen
                     challenged leaves (Pseudomonas syringae pv tomato 12 hr;
                     Xanthomonas campestris pv campestris 12 hr, 18hr;
                     Pseudomonas syringae pv phaseolicola 18hr, and Xanthomonas
                     campestris pv vesicatoria 18hr). RNA was isolated from
                     these tissues and pooled in approximately equal molar
                     amounts."
ORIGIN

Query Match         17.8%;   Score 939.4;  DB 7;  Length 954;
Best Local Similarity 99.9%;   Pred. No. 7.2e-259;
Matches 940;  Conservative 0;  Mismatches 0;  Indels 1;  Gaps 0;
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Qy   3991  AGATCCCGCGCTGGAGGATCATCCAGCCGGCGTCCCGGAAAACGATTCCGAAGCCCAAC  4050
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Db    954  AGATCCCGCGCTGGAGGATCATCCAGCCGGCGTCCCGGAAAACGATTCCGAAGCCCAAC  895

Qy   4051  CTTTCATAGAAGGCGGCCGGTGGAAATCTCGTGATGGCAGTTGGGCGTCGCTTGG  4110
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    894  CTTTCATAGAAGGCGGCCGGTGGAAATCTCGTGATGGCAGTTGGGCGTCGCTTGG  835

Qy   4111  TCGGTCATTCGAACCCAGAGTCCCGCTCAGAAGAACTCGTCAAGAAGGCGATAGAAG  4170
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    834  TCGGTCATTTCGAACCCAGAGTCCCGCTCAGAAGAACTCGTCAAGAAGGCGATAGAAG  775

Qy   4171  CGATGCGCTGCGAATCGGAGAGCGGCGATACCGTAAAGCACGAGAAGCCGGTCAGCCCATT  4230
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    774  CGATGCGCTGCGAATCGGAGAGCGGCGATACCGTAAAGCACGAGAAGCCGGTCAGCCCATT  715

Qy   4231  CGCCGCCAAGCTCTTCAGCAATATCACGGGTAGCCAACGCTATGTCCTGATAGCCGGTCCG  4290
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    714  CGCCGCCAAGCTCTTCAGCAATATCACGGGTAGCCAACGCTATGTCCTGATAGCCGGTCCG  655

Qy   4291  CCACACCCAGCCGGCCACAGTCGATGAATCCAGAAAAGCCGCCATTTTCCACCATGATAT  4350
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    654  CCACACCCAGCCGGCCACAGTCGATGAATCCAGAAAAGCCGCCATTTTCCACCATGATAT  595

Qy   4351  TCGGCAAGCAGGCATCGCCATGGTCACGACGAGATCCTCGCCGTCGGCGATGCGCGCCT  4410
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    594  TCGGCAAGCAGGCATCGCCATGGTCACGACGAGATCCTCGCCGTCGGCGATGCGCGCCT  535

Qy   4411  TGAGCCTGGCGAACAGTTCGGCTGGCGTGGCGGCGAGCCCCGAGCTCTTCGTCCAGATCATCCT  4470
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    534  TGAGCCTGGCGAACAGTTCGGCTGGCGTGGCGGCGAGCCCCGAGCTCTTCGTCCAGATCATCCT  475

Qy   4471  GATCGACAAGACCGGCTTCCATCCGAGTACGTCGCTGCTCGATGCGGATGTTTCGCTTGGT  4530
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    474  GATCGACAAGACCGGCTTCCATCCGAGTACGTCGCTGCTCGATGCGGATGTTTCGCTTGGT  415

Qy   4531  GGTCGAATGGGCAGGTAGCCGGATCAAGCCGGCGTATGCAGGCGCCGCATTGCATCAGCCATGA  4590
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    414  GGTCGAATGGGCAGGTAGCCGGATCAAGCCGGCGTATGCAGGCGCCGCATTGCATCAGCCATGA  355

Qy   4591  TGGATACTTTCTCGGCAGGAGCAAGGTGAGATGACAAGGAGAGATCCTGCCCGGCACTTCGC  4650
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    354  TGGATACTTTCTCGGCAGGAGCAAGGTGAGATGACAAGGAGAGATCCTGCCCGGCACTTCGC  295

Qy   4651  CCAATAGCAGCCAGTCCCTTCCCGCTTCAGTGACAACGTCGCGAGCACAGCTGCGCAAGGAA  4710
```

```
ACCESSION    AU081124
VERSION      AU081124.1  GI:6431472
KEYWORDS     EST.
SOURCE       Oncorhynchus mykiss (rainbow trout)
  ORGANISM   Oncorhynchus mykiss
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Actinopterygii; Neopterygii; Teleostei; Euteleostei;
             Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
REFERENCE    1  (bases 1 to 1089)
  AUTHORS    Kono,T., Sakai,M. and LaPatra,S.E.
  TITLE      Expressed Sequence Tag Analysis of Kidney and Gill Tissues from
             Rainbow Trout (Oncorhynchus mykiss) Infected with Infectious
             Hematopoietic Necrosis Virus
  JOURNAL    Mar. Biotechnol. 2 (5), 493-498 (2001)
COMMENT      Contact: Masahiro Sakai
             Faculty of Agriculture
             Miyazaki University
             1-1 nishi gakuenkibanadai, Miyazaki, Miyazaki 889-2192, Japan
             Email: m.sakai@cc.miyazaki-u.ac.jp.
FEATURES             Location/Qualifiers
     source          1..1089
                     /organism="Oncorhynchus mykiss"
                     /mol_type="mRNA"
                     /db_xref="taxon:8022"
                     /clone="KG'12"
                     /tissue_type="kidney"
                     /clone_lib="Oncorhynchus mykiss Kidney infected by
                     infectious hematopoietic necrosis virus"
                     /note="common name:rainbow trout ; infected by infectious
                     hematopoietic necrosis virus"

ORIGIN

Query Match             17.4%;   Score 919.8; DB 1;  Length 1089;
Best Local Similarity   97.3%;   Pred. No. 3.5e-253;
Matches  979;   Conservative    0;   Mismatches   22;   Indels    6;   Gaps    4;

Qy  2706 CTAGACGTAATCATGGTCATAGCTGTTTCCTGTGAAATTGTTATCCGCTCACAATTCC 2765
         |||||| |||||||||||||||||||||||||||||||||| ||||||||||||||||
Db    83 CTTGGGGTAATCATGGTCATAGCTGTTTCCTGTGAAATTGTTATCCGCTCACAATTCC  142

Qy  2766 ACACAACATACGAGCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTA 2825
         |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db   143 ACACAACATACGAGCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTA  202

Qy  2826 ACTCACATTAATTGCGTTGCGCTCACTGCGCCGGGGAAACCTGTCGTGCCA 2885
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   203 ACTCACATTAATTGCGTTGCGCTCACTGCGCCGGGGAAACCTGTCGTGCCA  262

Qy  2886 GCTGCATTAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTGCGTATTGGGGCGCTCTTC 2945
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   263 GCTGCATTAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTGCGTATTGGGGCGCTCTTC  322

Qy  2946 CGCTTCCTCGCTCACTGACCTGCTGCGGGCCGGCTCGGTCGTTCGGCTCGGCGGTATCAGC 3005
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   323 CGCTTCCTCGCTCACTGACCTGCTGCGGGCCGGCTCGGTCGTTCGGCTCGGCGGTATCAGC  382

Qy  3006 TCACTTCAAAGGCGGTAATACGGTTATCCAAGAATCAGGGGATAACGCCAGGAAAGAACAT 3065
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   383 TCACTTCAAAGGCGGTAATACGGTTATCCAAGAATCAGGGGATAACGCCAGGAAAGAACAT  442

Qy  3066 GTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTT 3125
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   443 GTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTT  502

Qy  3126 CCATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCG 3185
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   503 CCATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCG  562

Qy  3186 AAACCCGACAGGACTATAAAGATACCAGGCGTTCCCCCTGGAAGCTCCCTCGTGCGCTC 3245
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   563 AAACCCGACAGGACTATAAAGATACCAGGCGTTCCCCCTGGAAGCTCCCTCGTGCGCTC  622

Qy  3246 TCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGT 3305
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Matches  927;   Conservative    0;   Mismatches    4;   Indels    0;   Gaps    0;

Qy  4001 GCTGGGGATCATCCAGCCGCGGGTCCCGGAAAACGATTCCGAAGCCCAACCTTTCATAGA 4060
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   947 GCTGGAGGATCATCCAGCCGCGGGTCCCGGAAAACGATTCCGAAGCCCAACCTTTCATAGA  888

Qy  4061 AGGCGGCGGTGGAATCGAAATCTCGTGATGCCAGGTTGGGCGTCGCTTGGTCGTCATTT 4120
         |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db   887 AGGCGGCGGTGGAATCGAAATCTCGTGATGGCAGGTTGGGCGTCGCTGGTCGTCATTT  828

Qy  4121 CGAACCCCAGAGTCCCGCTCAGAAGAACTCGTCAAGAAGGCGATAGAAGGCGATGCGCTG 4180
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   827 CGAACCCCAGAGTCCCGCTCAGAAGAACTCGTCAAGAAGGCGATAGAAGGCGATGCGCTG  768

Qy  4181 CGAATCGGGAGCGGCGGCGATACCGTAAAGCACGAGGAGGCGGTCAGCCCATTCGCCGCAAG 4240
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   767 CGAATCGGGAGCGGCGGCGATACCGTAAAGCACGAGGAGGCGGTCAGCCCATTCGCCGCCAAG  708

Qy  4241 CTCTTCAGCAATATCACGGGTAGCCAACGTCTATGTCCTGATAGCGGTCCGCCACACCCAG 4300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   707 CTCTTCAGCAATATCACGGGTAGCCAACGTCTATGTCCTGATAGCGGTCCGCCACACCCAG  648

Qy  4301 CCGGCCACAGTCGATGAATCAGAAAAAGCGGCCATTTTCCACCATGATATTCGGCAAGCA 4360
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   647 CCGGCCACAGTCGATGAATCAGAAAAAGCGGCCATTTTCCACCATGATATTCGGCAAGCA  588

Qy  4361 GGCATCGGCCATGGGTCACGACGAGATCCTCGCCGTCGGCATGCGGCCTTGAGCCTGGC 4420
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   587 GGCATCGGCCATGGGTCACGACGAGATCCTCGCCGTCGGCATGCGGCCTTGAGCCTGGC  528

Qy  4421 GAACAGTTCGGCTGGCGGCGAGCCCCTGATGGCTCTTCGTCCAGATCATCCTGATCGACAAG 4480
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   527 GAACAGTTCGGCTGGCGGCGAGCCCCTGATGGCTCTTCGTCCAGATCATCCTGATCGACAAG  468

Qy  4481 ACCGGCTTCATCCGAGTACGTGCTCGCTCGCTCCGAGTACGTTCGCTTGGTGGTCGAATG 4540
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   467 ACCGGCTTCATCCGAGTACGTGCTCGCTCGCTCCGAGTACGTTCGCTTGGTGGTCGAATG  408

Qy  4541 GCAGGTAGCCGGATCAAGCGTATGCGCGCGCATTGCATCAGCCGCATGATGGATACTTT 4600
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   407 GCAGGTAGCCGGATCAAGCGTATGCGCGCGCATTGCATCAGCCGCATGATGGATACTTT  348

Qy  4601 CTCGGCAGGAGCAAGTGAGATGACAGAGAGATCCTCGCCCCGGCCACTTCGCCCAATAGCAG 4660
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   347 CTCGGCAGGAGCAAGTGAGATGACAGAGAGATCCTCGCCCCGGCCACTTCGCCCAATAGCAG  288

Qy  4661 CCAGTCCCTTCCCGCTTCAGTGACAACGTCGAGCAGTGCGCAAGGAACGCCCGTCGT 4720
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   287 CCAGTCCCTTCCCGCTTCAGTGACAACGTCGAGCAGTGCGCAAGGAACGCCCGTCGT  228

Qy  4721 GGCCAGCCACGATAGCCGCGCCCCTGCCCTGCGCGCTCGTCGTCCTGCAGTTCATTCAGGGCACCGGGAACACCGGCATCAGA 4780
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   227 GGCCAGCCACGATAGCCGCGCCCCTGCCCTGCGCGCTCGTCGTCCTGCAGTTCATTCAGGGCACCGGGAACACCGGCATCAGA  168

Qy  4781 GGTCTTGACAAAAAGAACACCGGGCGCCGCCCTGCGCTGACAGCCGGGACACCGGCGGCATCAGA 4840
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   167 GGTCTTGACAAAAAGAACACCGGGCGCCGCCCTGCGCTGACAGCCGGGACACCGGCGGCATCAGA  108

Qy  4841 GCAGCCGATTGTCTGTTGTGCCCAGTCATAGCCGAATAGCCTCTTCCACCCAAGCGGCCGG 4900
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   107 GCAGCCGATTGTCTGTTGTGCCCAGTCATAGCCGAATAGCCTCTTCCACCCAAGCGGCCGG  48

Qy  4901 AGAACCTGCGTGCAATCCATCTTGTTCAATC 4931
         |||||||||||||||||||||||||||||||
Db    47 AGAACCTGCGTGCAATCCATCCATCTTGTTCAATC  17
```

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RESULT 5
AU081124
LOCUS       AU081124                1089 bp    mRNA    linear   EST 30-JUL-2002
DEFINITION  AU081124 Oncorhynchus mykiss Kidney infected by infectious
            hematopoietic necrosis virus Oncorhynchus mykiss cDNA clone KG'12,
            mRNA sequence.
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grown plants, heat-stressed leaves (38 C, 3 hr and 6 hr),
cold-stressed leaves (5 C 3 hr, 6hr), and pathogen
challenged leaves (Pseudomonas syringae pv tomato 12 hr;
Xanthomonas campestris pv campestris 12 hr;
Pseudomonas syringae pv phaseolicola 18hr, and Xanthomonas
campestris pv vesicatoria 18hr). RNA was isolated from
these tissues and pooled in approximately equal molar
amounts."

ORIGIN

Query Match        17.4%;     Score 918.6;   DB 7;     Length 935;
Best Local Similarity  99.6%;   Pred. No. 7.3e-253;
Matches  921;   Conservative  0;   Mismatches  0;   Indels  4;   Gaps  0;

Qy  4030  AAAACGATTCCGAAGCCCAACCTTCATAGAAGGCGGCGGTGGAATCGAAATCTCGTGAT  4089
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   935  AAAACGATTCCGAAGCCCAACCTTTCATAGAAGGCGGCGGTGGAATCGAAATCTCGTGAT   876

Qy  4090  GGCAGGTTGGGCGTCGTTGGTCGGTCATTTCGAACCCCAGAGTCCCGCTCAGAAGAACT  4149
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   875  GGCAGGTTGGGCGTCGTTGGTCGGTCATTTCGAACCCCAGAGTCCCGCTCAGAAGAACT   816

Qy  4150  CGTCAAGAAGGCGATAGAAGGCGATCGCGTCGGAGGCGGCGATACCGTAAAGCA  4209
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   815  CGTCAAGAAGGCGATAGAAGGCGATGCGTCGGAGGCGGCGATACCGTAAAGCA   756

Qy  4210  CGAGGAAGCCGTCAGCCATTCGCCGCCAAGCTCTTCAGCAATATCACGGGTAGCCAACG  4269
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   755  CGAGGAAGCCGTCAGCCATTCGCCGCCAAGCTCTTCAGCAATATCACGGGTAGCCAACG   696

Qy  4270  CTATGTCCTGATAGCGGTCCGCCACACCCAGCCGGCCACAGTGAATCGATGAATCCAGAAAAGC  4329
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   695  CTATGTCCTGATAGCGGTCCGCCACACCCAGCCGGCCACAGTGAATCGATGAATCCAGAAAAGC   636

Qy  4330  GGCCATTTTCCACCATGATATTCGGCAAGCAGGCATCGCCAAGCGGTCACGACGAGATCCT  4389
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   635  GGCCATTTTCCACCATGATATTCGGCAAGCAGGCATCGCCAAGCGGTCACGACGAGATCAT   576

Qy  4390  CGCCGTCGGGCATGCGCCTTGAGCGTCGGCCTGGCGTGGCGCGCCCCGTGAT  4449
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   575  CGCCGTCGGGCATGCGCCTTGAGCGTCGGCCTGGCGTGGCGCGCCCCGTGAT   516

Qy  4450  GCTCTTCGTCCAGATCATCTCGATCGACAAGACCGGCTTCCATCCGAGTAGTGCTCGCT  4509
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   515  GCTCTTCGTCCAGATCATCTCGATCGACAAGACCGGCTTCCATCCGAGTAGTGCTCGCT   456

Qy  4510  CGATGCGATGTTTCGCTGGTGGTGAATGGCCAGTAGCCGGATCAAGCGTATGCGAGCC  4569
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   455  CGATGCGATGTTTCGCTGGTGGTGCAATGGCCAGTAGCCGGATCAAGCGTATGCGAGCC   396

Qy  4570  GCGAGCACAGCAGGCCATGATGGATACTTTCTCGGCAGGAGCAAGGTGAGATGACAGGA  4629
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   395  GCGCCGATTCAGCCATCAGCCGGCATCAGAGCAGCGATTGTCTGTTGTGCCCAGTCAT   336

Qy  4630  GATCCTGCCCCGGCCACTTCGCCCAATAGCAGCAGTTCCCTTCGCCGCTTCCCGTTCAGTGACAACGT  4689
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   335  GATCCTGCCCCGGCCACTTCGCCCAATAGCAGCAGTTCCCTTCGCCGCTTCCCGTTCAGTGACAACGT   276

Qy  4690  CGAGCACAGCAGGCTGCGCAAGGAACGCCCGTCGGCCACGATAGCCCGCTGCCTCGT  4749
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   275  CGAGCACAGCAGCTGCGCCAGGAACGCCCGTCGTCGGCCACGCCACGATAGCCCGCTGCCTCGT   216

Qy  4750  CCTGAGTTCATTCAGGGCACCGGACACCGGAGTCGGTCTTGACAAAAGAACCGGGCGCCCT  4809
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   215  CCTGAGTTCATTCAGGGCACCGGACACCGGAGTCGGTCTTGACAAAAGAACCGGGCGCCCCT   156

Qy  4810  GCGCTGACAGCCGGAACACGGCGCGCATCAGAGCAGCCGATTGTCTGTTGTGCCCAGTCAT  4869
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   155  GCGCTGACAGCCGGAACACGGCGCGCATCAGAGCAGCCGATTGTCTGTTGTGCCCAGTCAT    96

Qy  4870  AGCCGAATAGCCTTCTCCACCCAAGCCGCCGAGAACCTGCCTGCAATCCATCTTGTTCAA  4929
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    95  AGCCGAATAGCCTCTCCACCCAAGCCGCCGAGAACCTGCCTGCAATCCATCTTGTTCAA    36
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Db   623  |||||||||||||||||||||||||||||||||||||||||||||||||
          TCCTGTTCCGACCCTGCCGCTTACCCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGT   682

Qy  3306  GGCGCTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAA  3365
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   683  GGCGCTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAA   742

Qy  3366  GCTGGGCTGTGTGCACGAACCCCCGTTCAGCCGACCGGCTGCGGCCTTATCCGGTAACTA  3425
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   743  GCTGGGCTGTGTGCACGAACCCCCGTTCAGCCGACCGGCTGCGGCCTTATCCGGTAACTA   802

Qy  3426  TCGTTCTTGAGTCCAACCCGTAAGACACAGACTTATCGCCACTGGCAGCAGCCACTGGTAA  3485
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   803  TCGTTCTTGAGTCCAACCCGTAAGACACAGACTTATCGCCACTGGCAGCAGCCACTGGTAA   862

Qy  3486  CAGGATTAGCAGAGCGAGGTGTATGTAGGCCGGTGCTACAGAGTTCTTGAAG-TGGTTGGCCTA  3544
          |||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db   863  CAGGATTAGCAGAGCGAGGTGTATGTAGGCCGGTGCTACAGAGTTCTTGAAGTTGTTGGCCTA   922

Qy  3545  ACTACGGCTACACTAGAAGAAACAGTATTTGGTATCTCGCGCTCGCTGCTGAAGCCAGTTACCT  3604
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   923  ACTACGGCTACACTAGAAGAAACAGTATTTGTATCTGCGCTCGCTGGGAGCCAGTTACCT   982

Qy  3605  TCGGAAAAAGAGAGTTGGTAGCTCTT-GATCCGGCAAACAAACCA---CCGCTGGTAGCGGT  3660
          ||||||||||||||||||| |||||||||||||||||| |||||
Db   983  TCGGAAAAAGAGAGTGGGTAGCTCTTGGATCCGGCAAACAAACAACCGCTCGGAAGGGGGG  1042

Qy  3661  GGTTTTTGTTTTGCAAGCA-GCAGATTACGGCGCAGATTACCCCGCGAAAAAAGGAT  3706
          ||||||||||||||| ||||||||||||||||||| |||||
Db  1043  TGTCTTTTTGTTTTGCTTGCAAGCACGCAGATTACCCCGCGAAAAAAAACCGAT  1089
```

RESULT 6

CK284786/c

LOCUS   CK284786   935 bp   mRNA   linear   EST 02-AUG-2004
DEFINITION   EST747508 Nicotiana benthamiana mixed tissue cDNA library,
             normalized, full-length Nicotiana benthamiana cDNA clone NBMAQ41 5'
             end, mRNA sequence.
ACCESSION   CK284786
VERSION   CK284786.1 GI:39858698
KEYWORDS   EST.
SOURCE   Nicotiana benthamiana
  ORGANISM   Nicotiana benthamiana
             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
             Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
             asterids; lamiids; Solanales; Solanaceae; Nicotiana.
REFERENCE   1 (bases 1 to 935)
  AUTHORS   Buell,C.R., Hart,A., Zismann,V., Karamycheva,S.A., Day,B.,
             Staskawicz,B., Jin,H. and Baker,B.
  TITLE   Generation of EST sequences from Nicotiana benthamiana
  JOURNAL   Unpublished (2003)
COMMENT   Other ESTs: EST747509
             Contact: Robin Buell
             The Institute for Genomic Research
             9712 Medical Center Dr, Rockville, MD 20850, USA
             Email: potato-array@tigr.org
             Clones can be requested from the University of Arizona Genomics
             Institute via http://genome.arizona.edu/orders/ .
             Seq primer: ATT TAG GTG ACA CTA TAG.
FEATURES   Location/Qualifiers
     source   1..935
                     /organism="Nicotiana benthamiana"
                     /mol_type="mRNA"
                     /db_xref="taxon:4100"
                     /clone="NBMAQ41"
                     /tissue_type="abiotic and biotic stress-treated leaves,
                     callus tissue and root tissue"
                     /lab_host="DH10B-TonA"
                     /clone_lib="Nicotiana benthamiana mixed tissue cDNA
                     library, normalized, full-length"
                     /note="Vector: pCMVSport6.1; Site 1: EcoRI; Site 2: NotI;
                     supplier: RNA was isolated from Nicotiana benthamiana
                     tissues that include callus, roots from liquid culture

Qy   4369 CATGGGTCACGACGAGATCCTCGCGTCGCGGGCATGCGGCCTTGAGCCTGGCGAACAGTT 4428
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   576 CATGGGTCACGACGAGATCCTCGCGTCGCGGGCATGCGGCCTTGAGCCTGGCGAACAGTT 517

Qy   4429 CGGCTGGCGGCGGAGCCCCTGATGCTGTTCGTCGTCGTCCTCAGATCATCTGTCGTCGTT 4488
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   516 CGGCTGGCGGCGGAGCCCCTGATGCTGTTCGTCGTCGTCCTCAGATCATCTGTCGTCGTT 457

Qy   4489 CCATCCGAGTACGTGCTCGCTCGATGCGATGTTCGCTTGGTGGTCGATGGGCAGGTAG 4548
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   456 CCATCCGAGTACGTGCTCGCTCGATGCGATGTTCGCTTGGTGGTCGATGGGCAGGTAG 397

Qy   4549 CCGGATCAAGCGTATGCAGCCGCCGCATTGCATCAGCCATGATGGATACTTTCTCGGCAG 4608
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   396 CCGGATCAAGCGTATGCAGCCGCCGCATTGCATCAGCCATGATGGATACTTTCTCGGCAG 337

Qy   4609 GAGCAAGGTGAGATGACGAGAGAGATCCTGCCCCGGCACTTCGCCCAATAGCAGCCAGTCCC 4668
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   336 GAGCAAGGTGAGATGACGAGAGAGATCTGCCCCGGCACTTCGCCCAATAGCAGCCAGTCCC 277

Qy   4669 TTCCCGCTTCAGTGACAACGTCGAGCACAGCTGGCAAGGAACGCCCGTCGTGGCCAGCC 4728
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   276 TTCCCGCTTCAGTGACAACGTCGAGCACAGCTGGCAAGGAACGCCCGTCGTGGCCAGCC 217

Qy   4729 ACGATAGCCGGCTGCCTCGTCGTCCTCGCAGTTCATTCAGGGCACCGGACAGGTCGGTCTTGA 4788
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   216 ACGATAGCCGGCTGCCTCGTCGTCCTCGCAGTTCATTCAGGGCACCGGACAGGTCGGTCTTGA 157

Qy   4789 CAAAAAGAACCGGGCGCCCCCTGCGTGACAGCCGGAACACGGCGGGCATCAGAGCAGCGA 4848
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   156 CAAAAAGAACCGGGCGCCCCCTGCGTGACAGCCGGAACACGGCGGGCATCAGAGCAGCCGA 97

Qy   4849 TTGTCGTGTGTGCCCAGTCATAGCCGAATAGCCTCTCCACCCAAGCGGCCGGAGAACCTG 4908
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   96 TTGTCGTGTGTGCCCAGTCATAGCCGAATAGCCTCTCCACCCAAGCGGCCGGAGAACCTG 37

Qy   4909 CGTGCAATCCATCTTGTTCAATC 4931
           |||||||||||||||||||||||
Db   36 CGTGCAATCCATCTTGTTCAATC 14

RESULT 8
CK287930/c
LOCUS   CK287930   910 bp   mRNA   linear   EST 02-AUG-2004
DEFINITION   EST750652 Nicotiana benthamiana mixed tissue cDNA library,
               normalized, full-length Nicotiana benthamiana cDNA clone NBMBC75 5'
               end, mRNA sequence.
ACCESSION   CK287930
VERSION   CK287930.1   GI:39864940
KEYWORDS   EST.
SOURCE   Nicotiana benthamiana
ORGANISM   Nicotiana benthamiana
               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
               Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
               asterids; lamiids; Solanales; Solanaceae; Nicotiana.
REFERENCE   1 (bases 1 to 910)
AUTHORS   Buell,C.R., Hart,A., Zismann,V., Karamycheva,S.A., Day,B.,
               Staskawicz,B., Jin,H. and Baker,B.
TITLE   Generation of EST sequences from Nicotiana benthamiana
JOURNAL   Unpublished (2003)
COMMENT   Other_ESTs: EST75653
               Contact: Robin Buell
               The Institute for Genomic Research
               9712 Medical Center Dr. Rockville, MD 20850, USA
               Email: potato-array@tigr.org
               Clones can be requested from the University of Arizona Genomics
               Institute via http://genome.arizona.edu/orders/ .
               Seq primer: ATT TAG GTG ACA CTA TAG.
FEATURES   Location/Qualifiers
source   1..910
               /organism="Nicotiana benthamiana"
               /mol_type="mRNA"

Qy   4930 TCATGCCGAAACGATCCTCATCCTGT 4954
           |||||||||| ||||| |||| ||
Db   35 TCATGCCGAAACGATCCAGATCCGGT 11

RESULT 7
CK256977/c
LOCUS   CK256977   936 bp   mRNA   linear   EST 30-JUL-2004
DEFINITION   EST740614 potato callus cDNA library, normalized and full-length
               Solanum tuberosum cDNA clone POCD170 5' end, mRNA sequence.
ACCESSION   CK256977
VERSION   CK256977.1   GI:39813957
KEYWORDS   EST.
SOURCE   Solanum tuberosum (potato)
ORGANISM   Solanum tuberosum
               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
               Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
               asterids; lamiids; Solanales; Solanaceae; Solanum.
REFERENCE   1 (bases 1 to 936)
AUTHORS   Buell,C.R., Hart,A., Zismann,V., Karamycheva,S.A. and Baker,B.
TITLE   Generation of ESTs from potato callus tissue
JOURNAL   Unpublished (2003)
COMMENT   Contact: Robin Buell
               The Institute for Genomic Research
               9712 Medical Center Dr, Rockville, MD 20850, USA
               Email: potato-array@tigr.org
               Clones can be requested from the University of Arizona Genomics
               Institute via http://genome.arizona.edu/orders/ .
               Seq primer: ATT TAG GTG ACA CTA TAG.
FEATURES   Location/Qualifiers
source   1..936
               /organism="Solanum tuberosum"
               /mol_type="mRNA"
               /cultivar="Kennebec"
               /db_xref="taxon:4113"
               /clone="POCD170"
               /tissue_type="callus"
               /lab_host="DH10B-TonA"
               /clone_lib="potato callus cDNA library, normalized and
               full-length"
               /note="Vector: pCMVSport6.1; Site 1: EcoRI; Site 2: NotI;
               supplier: pCMVSport6.1; RNA was isolated from Solanum tuberosum var.
               Kennebec callus tissue grown on solid media."

ORIGIN
Query Match   17.2%; Score 911; DB 7; Length 936;
Best Local Similarity 99.9%; Pred. No. 1.1e-250;
Matches 922   Conservative   0; Mismatches   0; Indels   1; Gaps   1;

Qy   4010 TCATCCAGCCGGCCGTCCC-GGAAAACGAGATTCCGAAGCCCAACCTTCATAGAAGCGCGGCG 4068
           ||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db   936 TCATCCAGCCGGCCGTCCCGGGAAAACGAGATTCCGAAGCCCAACCTTCATAGAAGCGCGGCG 877

Qy   4069 GTGGAATCGAAATCTCGTGATGGCAGGTTGGGCGTCGGTCGTCGGTCATTTCGAACCCC 4128
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   876 GTGGAATCGAAATCTCGTGATGGCAGGTTGGGCGTCGGTCGTCGGTCATTTCGAACCCC 817

Qy   4129 AGAGTCCGCTCAGAAGAACTCGTCAAGAAGGCGATAGAGAGGCGATGGCGCTGCGAATCGG 4188
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   816 AGAGTCCGCTCAGAAGAACTCGTCAAGAAGGCGATAGAGAGGCGATGGCGCTGCGAATCGG 757

Qy   4189 GAGCGGCGGATACCGTAAAGCACGAGGAAGCCGGTCAGCCCATTCGCCGCCAAGCTCTTCAG 4248
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   756 GAGCGGCGGATACCGTAAAGCACGAGGAAGCCGGTCAGCCCATTCGCCGCCAAGCTCTTCAG 697

Qy   4249 CAATATCACGGGTAGCCAACGCTATGTCCTGATAGCGGTCCGCCACACCCAGCCGCCAC 4308
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   696 CAATATCACGGGTAGCCAACGCTATGTCCTGATAGCGGTCCGCCACACCCAGCCGCCAC 637

Qy   4309 AGTCGATGAATCCAGAAAAGCGGCAAAAGCGGCCATTTTCCACCATGATAATTCGGCAAGCAGGCATCGC 4368
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   636 AGTCGATGAATCCAGAAAAGCGGCCATTTTCCACCATGATAATTCGGCAAGCAGGCATCGC 577

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Db    190 CTGCTTCTGCAGTTCATTCAGGGCACCGGACCAGCAGTCGGTCTTGACAAAAGAACGGGCG 131
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4805 CCCCTGCGCTGACAGCCGGAACACGGCGGCATCAGCGCAGCGGATTGTCTGTTGTGCCCA 4864
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    130 CCCCTGCGCTGACAGCCGGAACACGGCGGCATCAGCGCAGCGGATTGTCTGTTGTGCCCA 71
Qy   4865 GTCATAGCGGAATAGCCTCTCCACCCAAGCGGCCGGAGAACCTGCGTGCAATCCATCTTG 4924
          ||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Db     70 GTCATAGCCGAATAGCCTCTCCACCCAAGCGGCCGGAGAACCTGCGTGCAATCCATCTTG 11
Qy   4925 TTCAATC 4931
          |||||||
Db     10 TTCAATC 4
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RESULT 9
CL021189

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LOCUS       CL021189              1049 bp    DNA     linear   GSS 31-DEC-2003
DEFINITION  CH216-8A14_RM1.1 CH216 Xenopus tropicalis genomic clone CH216-8A14,
            genomic survey sequence.
ACCESSION   CL021189
VERSION     CL021189.1  GI:40463002
KEYWORDS    GSS.
SOURCE      Xenopus tropicalis (western clawed frog)
  ORGANISM  Xenopus tropicalis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
            Xenopodinae; Xenopus; Silurana.
REFERENCE   1  (bases 1 to 1049)
  AUTHORS   Kremitzki,C., Carter,J., McPherson,J., Warren,W., Graves,T.,
            Mardis,E. and Wilson,R.
  TITLE     A physical map of the xenopus tropicalis genome
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Richard K Wilson
            Genome Sequencing Center
            Washington University School of Medicine
            Email: submissions@watson.wustl.edu
            Insert Length: 175000    Std Error: 0.00
            Seq primer: RM1 TACGACTCACTATAGGGAGA
            Class: BAC ends
            High quality sequence start: 43
            High quality sequence stop: 888.
FEATURES             Location/Qualifiers
     source          1..1049
                     /organism="Xenopus tropicalis"
                     /mol_type="genomic DNA"
                     /strain="Nigerian frog"
                     /db_xref="taxon:8364"
                     /clone="CH216-8A14"
                     /sex="male"
                     /cell_line="Stock 248 F7A2, inbred N7"
                     /clone_lib="CH216"
                     /note="Vector: pTARBAC2.1; CHORI-216 Xenopus tropicalis
                     BAC library"
ORIGIN
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Query Match     17.0%;   Score 897.4;   DB 9;   Length 1049;
Best Local Similarity   98.1%;   Pred. No. 1e-246;
Matches  929;   Conservative   0;   Mismatches  16;   Indels   2;   Gaps  2;
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Qy   2701 GCTGTCTAGACGTAATCATGGTCATCAGCTGTTTCCTGTGTGGAAATTGTTATCCGCTCACA 2760
          ||||  |||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db    102 GCAAGCTTGGCGTAATCATGTCATCAGCTGTTTCCTGTGTGGAAATTGTTATCCGCTCACA 161
Qy   2761 ATTCCACAACACATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTG 2820
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    162 ATTCCACAACACATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTG 221
Qy   2821 AGCTAACTCACATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCG 2880
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    222 AGCTAACTCACATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCG 281
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            /db_xref="taxon:4100"
            /clone="NBMBC75"
            /tissue_type="abiotic and biotic stress-treated leaves,
            callus tissue and root tissue"
            /lab_host="DH10B-TonA"
            /clone_lib="Nicotiana benthamiana mixed tissue cDNA
            library, normalized, full-length"
            /note="Vector: pCMVSport6.1; Site_1: EcoRI; Site_2: NotI;
            supplier: RNA was isolated from Nicotiana benthamiana
            tissues that include callus, roots from liquid culture
            grown plants, heat-stressed leaves (38 C, 3 hr and 6 hr),
            cold-stressed leaves (5 C 3 hr, 6hr), and pathogen
            challenged leaves (Pseudomonas syringae pv tomato 12 hr;
            Xanthomonas campestris pv campestris 12 hr, 18hr;
            Pseudomonas syringae pv phaseolicola 18hr, and Xanthomonas
            campestris pv vesicatoria 18hr). RNA was isolated from
            these tissues and pooled in approximately equal molar
            amounts."
ORIGIN
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Query Match     17.2%;   Score 907;   DB 7;   Length 910;
Best Local Similarity   100.0%;   Pred. No. 1.6e-249;
Matches  907;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps  0;
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Qy   4025 CCCGAAACGATTCCGAAGCCCAACCTTTCATAGAAGGGCGGTGGAATCGAAATCTC 4084
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Db    910 CCCGAAACGATTCCGAAGCCCAACCTTTCATAGAAGGGCGGTGGAATCGAAATCTC 851
Qy   4085 GTGATGGCAGGTTGGGCGTCGGTTGGCTTGGTCGGTCATTTGAACCCCAGAGTCCCGCTCAGAA 4144
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    850 GTGATGGCAGGTTGGGCGTCGGTTGGCTTGGTCGGTCATTTGAACCCCAGAGTCCCGCTCAGAA 791
Qy   4145 GAACTCGTCAAGAAGGCGATAGAAGGCGATGCGCTGCGAATCGGGAGCCGGCGATACCGTA 4204
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    790 GAACTCGTCAAGAAGGCGATAGAAGGCGATGCGCTGCGAATCGGGAGCCGGCGATACCGTA 731
Qy   4205 AAGCACGAGGAGAGCCGGTCAGCCATTCGCCGCCAAGCTCTTCAGCAATATCACGGGTAGC 4264
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    730 AAGCACGAGGAGAGCCGGTCAGCCATTCGCCGCCAAGCTCTTCAGCAATATCACGGGTAGC 671
Qy   4265 CAACGCTATGTCCTGATAGCGGTCCGCCCACACCCAGCCGGCCACAGTCGATGAATCCAGA 4324
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    670 CAACGCTATGTCCTGATAGCGGTCCGCCCACACCCAGCCGGCCACAGTCGATGAATCCAGA 611
Qy   4325 AAAGGCGGCCATTTTCCACCATGATATTCGGCAAGCAGGCATCGCCATGGGTCACGACGAG 4384
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Db    610 AAAGGCGGCCATTTTCCACCATGATATTCGGCAAGCAGGCATCGCCATGGGTCACGACGAG 551
Qy   4385 ATCCTCCGCCCTCGGGGATGCGCGCTTGAGCCTGGCGAACAGTTCGGCGTGGCGGCAGCCC 4444
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    550 ATCCTCCGCCCTCGGGGATGCGCGCTTGAGCCTGGCGAACAGTTCGGCGTGGCGGCAGCCC 491
Qy   4445 CTGATGCTCTTCGTCCAGATCATCCTGATCGACAAGACCCGCTTCCATCCGAGTACGTGC 4504
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    490 CTGATGCTCTTCGTCCAGATCATCCTGATCGACAAGACCCGCTTCCATCCGAGTACGTGC 431
Qy   4505 TCGCTCGATGCGATGTTTCGCTTGGTGGTCGAATGGGCAGGTAGCCGGATCAAGGCGTATG 4564
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    430 TCGCTCGATGCGATGTTTCGCTTGGTGGTCGAATGGGCAGGTAGCCGGATCAAGGCGTATG 371
Qy   4565 CAGCCGCCGCATTCAGCGATGGATACTTTCTCGGCAGGAGCAAGGTGAGATGA 4624
          ||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db    370 CAGCCGCCGCATTGCATCAGCGATGGATACTTTCTCGGCAGGAGCAAGGTGAGATGA 311
Qy   4625 CAGGAGATCCGCCCCGGACTTCGCCCAATAGCAGCCAGTCCCTTCCCGCTTCAGTGAC 4684
          |||||||||| ||||||| ||| |||||||||||||||||||||||||||||||||
Db    310 CAGGAGATCCTGCCCCGGCACTTGGCCAATAGCAGCCAGTCCCTTCCCGCTTCAGTGAC 251
Qy   4685 AACGTCGAGCACAGCTGCGCAAGGAACGCCGTCGTGGCCCAGCCACGATAGCCCGGCTGC 4744
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    250 AACGTCGAGCACAGCTGCGCAAGGAACGCCGTCGTGGCCCAGCCACGATAGCCCGGCTGC 191
Qy   4745 CTCGTCCTCGCAGTTCATTCAGGGCACCGGACCAGGTCGGTCTTGACAAAAGAACGGGCG 4804
```

```
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@tigr.org
Clones can be requested from the University of Arizona Genomics
Institute via http://genome.arizona.edu/orders/.
Seq primer: ATT TAG GTG ACA CTA TAG.

FEATURES        Location/Qualifiers
     source     1..933
                /organism="Nicotiana benthamiana"
                /mol_type="mRNA"
                /db_xref="taxon:4100"
                /clone="NBMC477"
                /tissue_type="abiotic and biotic stress-treated leaves,
                callus tissue and root tissue"
                /clone_lib="Nicotiana benthamiana mixed tissue cDNA
                library, normalized, full-length"
                /note="Vector: pCMVSport6.1; Site_1: EcoRI; Site_2: NotI;
                supplier: RNA was isolated from Nicotiana benthamiana
                tissues that include callus, roots from liquid culture
                grown plants, heat-stressed leaves (38 C, 3 hr and 6 hr),
                cold-stressed leaves (5 C 3 hr, 6hr), and pathogen
                challenged leaves (Pseudomonas syringae pv tomato 12 hr,
                Xanthomonas campestris pv campestris 12 hr, 18hr;
                Pseudomonas syringae pv phaseolicola 18hr, and Xanthomonas
                campestris pv vesicatoria 18hr). RNA was isolated from
                these tissues and pooled in approximately equal molar
                amounts."
ORIGIN

Query Match       16.8%;  Score 886.4;  DB 7;  Length 933;
Best Local Similarity 99.9%;  Pred. No. 1.4e-243;
Matches  887;  Conservative  0;  Mismatches  1;  Indels  0;  Gaps  0;
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Qy 4044 GCCCAACCTTCATAGAAGCGGCGGTGGAATCGTGATGCAGTTGGGCGT 4103
        ||||||||||||||||||||||||||||||||||||||||||||||||
Db  933 GCCCAACCTTCATAGAAGCGGCGGTGGAATCGTGATGCAGTTGGGCGT  874

Qy 4104 CGCTTGGTCGGTCATTTCGAACCCCAGAGTCGCTCAGAAGAACTCGTCAAGAAGGGA 4163
        ||||||||||||||||||||||||||||||||||||||||||||||||
Db  873 CGCTTGGTCGGTCATTTCGAACCCCAGAGTCGCTCAGAAGAACTCGTCAAGAAGGGA  814

Qy 4164 TAGAAGGCGATGCGCTGCGAATCGGGAGCGGCGGCGATACCGTAAAGCACGAGGAAGCGGGTCA 4223
        ||||||||||||||||||||||||||||||||||||||||||||||||
Db  813 TAGAAGGCGATGCGCTGCGAATCGGGAGCGGCGGCGATACCGTAAAGCACGAGGAAGCGGGTCA  754

Qy 4224 GCCCATTCGCCGCCAAGCTCTTCAGCAATATCACGGTAGCCAACGTATGTCCTGATAG 4283
        ||||||||||||||||||||||||||||||||||||||||||||||||
Db  753 GCCCATTCGCCGCCAAGCTCTTCAGCAATATCACGGTAGCCAACGTATGTCCTGATAG  694

Qy 4284 CGGTCCGCCGCACACCCAGCCGGCCACAGTCGATGAATCCAGAAAAGCCGGCCATTTCCACC 4343
        ||||||||||||||||||||||||||||||||||||||||||||||||
Db  693 CGGTCCGCCGCACACCCAGCCGGCCACAGTCGATGAATCCAGAAAAGCCGGCCATTTCCACC  634

Qy 4344 ATGATATTCGGCAAGCAGGCATCGCACGACGAGATCCTCGCCGGTCGGGCATG 4403
        ||||||||||||||||||||||||||||||||||||||||||||||||
Db  633 ATGATATTCGGCAAGCAGGCATCGCACGACGAGATCCTCGCCGGTCGGGCATG  574

Qy 4404 CCGGCCTTGAGCGTTGCGCGAACAGTTCGGCGTGCTGGCGCGAGCCCCGTCTTCGTCCAGA 4463
        ||||||||||||||||||||||||||||||||||||||||||||||||
Db  573 CCGGCCTTGAGCGTTGCGCGAACAGTTCGGCGTGCTGGCGCGAGCCCCGTCTTCGTCCAGA  514

Qy 4464 TCATCCTGATCGACAAGACCGGCTTCCATCCGGATCAAGCGTATGCAGTGCTCGCGATGTTC 4523
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Db  513 TCATCCTGATCGACAAGACCGGCTTCCATCCGGATCAAGCGTATGCAGTGCTCGCGATGTTC  454

Qy 4524 GCTTGGTGGTCGAATGGGCAGTAGCCGGATCAAGCGTATGCAGTGCTCGCGATCATCA 4583
        ||||||||||||||||||||||||||||||||||||||||||||||||
Db  453 GCTTGGTGGTCGAATGGGCAGTAGCCGGATCAAGCGTATGCAGTGCTCGCGATCATCA  394

Qy 4584 GCCATGATGGATACTTTCTCGGACAGGACGCAAGTGAGATGACGAGAGCAGGAGATCCTCGCCCGGC 4643
        ||||||||||||||||||||||||||||||||||||||||||||||||
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Qy 2881 TGCCAGCTGCATTAATGAATCGGCCAACGCGCGGGAGAGGCGGTTTGCGTATTGGGCGC 2940
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Db  282 TGCCAGCTGCATTAATGAATCGGCCAACGCGCGGGAGAGGCGGTTTGCGTATTGGGCGC  341

Qy 2941 TCTTCCGCTTCCTCGCTCACTGACTCGCTCGTTCGGCTGCGGCGAGCCGTA 3000
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Db  342 TCTTCCGCTTCCTCGCTCACTGACTCGCTCGTTCGGCTCGCGGCGAGCCGTA  401

Qy 3001 TCAGCTCACTCAAAGGCGTAATACGGTTATCCACAGAATCAGGGATAACGCAGGAAAG 3060
        ||||||||||||||||||||||||||||||||||||||||||||||||
Db  402 TCAGCTCACTCAAAGGCGTAATACGGTTATCCACAGAATCAGGGATAACGCAGGAAAG  461

Qy 3061 AACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCG 3120
        ||||||||||||||||||||||||||||||||||||||||||||||||
Db  462 AACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCG  521

Qy 3121 TTTTTCCATAGGCTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGG 3180
        ||||||||||||||||||||||||||||||||||||||||||||||||
Db  522 TTTTTCCATAGGCTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGG  581

Qy 3181 TGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTG 3240
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Db  582 TGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTG  641

Qy 3241 CGCTCTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGA 3300
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Db  642 CGCTCTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGA  701

Qy 3301 AGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGC 3360
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Db  702 AGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGC  761

Qy 3361 TCCAAGCTGGGCTGTGTGCACGAACCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGT 3420
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Db  762 TCCAAGCTGGGCTGTGTGCACGAACCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGT  821

Qy 3421 AACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACT 3480
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Db  822 AACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACT  881

Qy 3481 GGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGG 3540
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Db  882 GGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGG  941

Qy 3541 CCTAACTACGGCTACACTAGAAGAAC-AGTATTTGGTATCTGCGCCTGCTGAAGCCAGT 3599
        |||||||||||||||||||||||| |||||||||||||||||||||||
Db  942 CCTAACTACGGCTACACTAGAAGAACAAGTATTTGTTATCTGCGCTCTGCTGAAACCAGT 1001

Qy 3600 TACC-TTCGGAAAAAAGAGTTGGTAGCTTCTTGATCCGGCAAACAAAC 3645
        |||| ||||||| ||||||||||||||||| |  | | |||
Db 1002 TACCTTTCGGAAAAAAGTTGGTAGCTTCTTGAATCCGGCAAAAAAAC 1048
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RESULT 10
CK291799/c

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LOCUS       CK291799   933 bp   mRNA   linear   EST 02-AUG-2004
DEFINITION  EST754513 Nicotiana benthamiana mixed tissue cDNA library,
            normalized, full-length Nicotiana benthamiana cDNA clone NBMC477 5'
            end, mRNA sequence.
ACCESSION   CK291799
VERSION     CK291799.1  GI:39872608
KEYWORDS    EST.
SOURCE      Nicotiana benthamiana
  ORGANISM  Nicotiana benthamiana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            asterids; lamiids; Solanales; Solanaceae; Nicotiana.
REFERENCE   1  (bases 1 to 933)
  AUTHORS   Buell,C.R., Hart,A., Zismann,V., Karamycheva,S.A., Day,B.,
            Staskawicz,B., Jin,H. and Baker,B.
  TITLE     Generation of EST sequences from Nicotiana benthamiana
  JOURNAL   Unpublished (2003)
COMMENT     Other_ESTs: EST754514
```

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Db   393 GCCATGATGGATACTTTCTCGCAGGAGCAAGGTGAGATGACAGGAGATCCTGCCCGGC 334

Qy  2701 GCTGTCTAGACGTAATCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACA 2760
             ||||||||||||||||||||||||||||||||||||  |||||| ||||||| |||||
Db   898 GCGCGCTTGGCTAATCATCATGTCATAGCTGTTT-CTGTGTGAAATTGTTATCCGCTCACA 840

Qy  4644 ACTTCGCCAATAGCAGCCAGTCCCTTCCCGCTTCAGTGACAACGTCGAGCACAGCTGCG 4703
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   333 ACTTCGCCAATAGCAGCCAGTCCCTTCCCGCTTCAGTGACAACGTCGAGCACAGCTGCG 274

Qy  2761 ATTCCACACAACATACGAGCCGGAAGCATAAAGTAAAGCTCGGGGTGCCTAATGAGTG 2820
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   839 ATTCCACACAACATACGAGCCGGAAGCATAAAGTAAAGCTCGGGGTGCCTAATGAGTG 780

Qy  4704 CAAGGAACGCCCGTCGTGGCCAGCCACGATAGCCCGCTTCAGTTCATTC 4763
             |||||||||||||||||||||||||||||||||||||||||||||||||
Db   273 CAAGGAACGCCCGTCGTGGCCAGCCACGATAGCCCGCTTCAGTTCATTC 214

Qy  2821 AGCTAACTCACATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCG 2880
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   779 AGCTAACTCACATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCG 720

Qy  4764 AGGGCACCCGACAGTTCGGTCTTGACAAAAAGAACCGGAGCCCCTGCGGTCGACAGCCGG 4823
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   213 AGGGCACCCGACAGTTCGGTCTTGACAAAAAGAACCGGGGCCCCTGCGGTCGACAGCCGG 154

Qy  2881 TGCCAGCTGCATTAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGC 2940
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   719 TGCCAGCTGCATTAATGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGC 660

Qy  4824 AACACGGCGGCATCAGAGCAGCAGCCGATTGTCGTTGTGCCCAGTCATAGCCGAATAGCCTC 4883
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   153 AACACGGCGGCATCAGAGCAGCAGCCGATTGTCGTTGTGCCCAGTCATAGCCGAATAGCCTC 94

Qy  2941 TCTTCCGCTTCCTCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTA 3000
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   659 TCTTCCGCTTCCTCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTA 600

Qy  4884 TCCACCCAAGGGGCCGGAGAACCTGCGTGCGAATCCATCTTGTTCAATC 4931
             |||||||||||||||||||||||||||||||||||||||||||||||||
Db    93 TCCACCCAAGGCGGCCGGAGAACCTGCGTGCGAATCCATCTTGTTCAATC 46

Qy  3001 TCAGCTCACTCAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAG 3060
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   599 TCAGCTCACTCAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAG 540

Qy  3061 AACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCG 3120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   539 AACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGGG 480

Qy  3121 TTTTTCCATAGGCTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGG 3180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   479 TTTTTCCATAGGCTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGG 420

Qy  3181 TGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTG 3240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   419 TGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTG 360

Qy  3241 CGCTCTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGA 3300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   359 CGCTCTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGA 300

Qy  3301 AGGGTGGCGCTTTCTCATAGTCACGCTGTAGGTATCCAGTTCGGTGTAGGTCGTTCGC 3360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   299 AGCGTGGCGCTTTCTCATAGTCACGCTGTAGGTATCCAGTTCGGTGTAGGTCGTTCGC 240

Qy  3361 TCCAAGCTGGGCTGTGTGCACGAACCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGT 3420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||::
Db   239 TCCAAGCTGGGCTGTGTGCACGAACCCCCGTTCAGCCCGACCGCTGCGGCCTTATCCGGT 180

Qy  3421 AACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACT 3480
             ||||||||||||||||::||||||||||||||||||||||||::||||||||||||||
Db   179 AACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGSAGCAGCCACT 120

Qy  3481 GGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGG 3540
             |||||||||||||||||||||||||::||||||||||||||||||||::||||||||||
Db   119 GGTAACARGATTASCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTSAAGTGGTGG 60

Qy  3541 CCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCGCGCTCTGCGAAGCCAGT 3599
             ||||||||  ||||||||||||||||||||||||||||||||||||||||||||||
Db    59 CTTAACTACGGSTACACTAGAAGAACAGTATTTGGTATCGCGCTCTGCTGCGAAGCCAGT 1
```

RESULT 11
CB686151/c
LOCUS   CB686151   925 bp   mRNA   linear   EST 09-APR-2003
DEFINITION Bn01b_02oO8_A
            Bn01b AAFC_ECORC transgenic Brassica napus overexpressing BNCBF17_c
            onstitutively_frost_tolerant Brassica napus cDNA clone Bn01b_02oO8,
            mRNA sequence.
ACCESSION   CB686151
VERSION   CB686151.1 GI:29689876
KEYWORDS   EST.
SOURCE   Brassica napus (rape)
  ORGANISM Brassica napus
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE   1 (bases 1 to 925)
  AUTHORS   Singh,J., Allard,G., Tinker,N., Robert,L., Lacroix,C., De Moors,A.,
            Chagnon,J. Farah.S., Couroux,P. and Hattori,J.
  TITLE   Expressed Sequence Tags from constitutively frost tolerant
            transgenic Brassica napus overexpressing BNCBF17
  JOURNAL   Unpublished (2002)
COMMENT   Contact: Singh,J.A.
            Eastern Cereal and Oilseed Research Centre
            Agriculture and Agri-food Canada
            KW Neatby Bldg., Central Experimental Farm, Ottawa, Ontario, K1A
            OC6, Canada
            Tel: (613) 759-1662
            Fax: (613) 759-1701
            Email: singhja@agr.gc.ca.
FEATURES   Location/Qualifiers
     source   1..925
                     /organism="Brassica napus"
                     /mol_type="mRNA"
                     /cultivar="Westar"
                     /db_xref="taxon:3708"
                     /clone="Bn01b_02oO8"
                     /tissue_type="fourth leaf"
                     /dev_stage="3 weeks seedling grown at room temperature"
                     /clone_lib="Bn01b AAFC_ECORC transgenic_Brassica_napus_ove
                     rexpressing_BNCBF17_constitutively_frost_tolerant"
                     /note="Vector: Bluescript SK+/XhoI-EcoRI; Site 1: EcoRI;
                     Site 2: XhoI; Germinated in soil flats and seedlings grown
                     for 3 weeks in a Conviron E-15 cabinet set at 20oC /16 hr
                     light (250 Em-2sec-1) and 16 oC / 8 hr dark. Fourth leaves
                     collected at 9 am and immediately frozen."
ORIGIN

Query Match   16.6%;   Score 875;   DB 6;   Length 925;
Best Local Similarity 98.6%;   Pred. No. 2.8e-240;
Matches 886;   Conservative   6;   Mismatches   6;   Indels   1;   Gaps   1;

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Qy  3481 GGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGG 3540
```

RESULT 12
CF269652
LOCUS   CF269652   1073 bp   mRNA   linear   EST 13-AUG-2003
DEFINITION Fcylcold844 Fragilariopsis cylindrus SMART cDNA library (Clontech)
            Fragilariopsis cylindrus cDNA clone Antarctic 5', mRNA sequence.
ACCESSION   CF269652
VERSION   CF269652.1 GI:33631539
KEYWORDS   EST.
SOURCE   Fragilariopsis cylindrus
  ORGANISM Fragilariopsis cylindrus
            Eukaryota; stramenopiles; Bacillariophyta; Bacillariophyceae;

```
REFERENCE    1 (bases 1 to 1073)
  AUTHORS    Mock,T. and Valentin,K.
  TITLE      EST analysis of freezing tolerance in the Antarctic diatom
             Fragilariopsis cylindrus: Detection of numerous cold adaption
             related genes and gene transfer events
  JOURNAL    Unpublished (2003)
  COMMENT    Contact: Mock T
             Biological Oceanography
             Alfred-Wegener-Intitute for Polar and Marine Research
             Am Handelshafen 12, D-27570 Bremerhaven, Germany
             Tel: +49 471 4831 1893
             Fax: +49 471 4831 1425
             Email: tmock@awi-bremerhaven.de
             PCR PRimers
             FORWARD: 5'lambdaTriplEX2
             BACKWARD: 3'lambdaTriplEX2
             Seq primer: ctcggaagcggccattgtgttggt.
  FEATURES             Location/Qualifiers
       source          1..1073
                       /organism="Fragilariopsis cylindrus"
                       /mol_type="mRNA"
                       /strain="Antarctic"
                       /db_xref="taxon:186039"
                       /clone="Antarctic"
                       /clone_lib="Fragilariopsis cylindrus SMART cDNA library
                       (Clontech)"
                       /note="Vector: pTriplEX2; total polyA was used for
                       first-strand synthesis with SMART IV oiligos and CDS
                       III/3'PCR primer. Double strand cDNA synthesis was done by
                       LD PCR using the following program: 95oC for 5 min
                       denaturation and subsequent 20 cycles at 95oC (2min) and
                       68oC (6min). After SfiI digestion the cDNA was
                       fractionated with CHROMA Spin-400 columns. These cDNAs
                       were ligated overnight into pTriplEX2 vectors."
```

(sequence alignment data)

```
RESULT 13
CL076016
  LOCUS       CL076016                 885 bp    DNA     linear   GSS 31-DEC-2003
  DEFINITION  CH216-138F20_RM1.1 CH216 Xenopus tropicalis genomic clone
              CH216-138F20, genomic survey sequence.
  ACCESSION   CL076016
  VERSION     CL076016.1  GI:40531929
  KEYWORDS    GSS.
  SOURCE      Xenopus tropicalis (western clawed frog)
    ORGANISM  Xenopus tropicalis
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
              Xenopodinae; Xenopus; Silurana.
  REFERENCE   1 (bases 1 to 885)
    AUTHORS   Kremitzki,C., Carter,J., McPherson,J., Warren,W., Graves,T.,
              Mardis,E. and Wilson,R.
    TITLE     A physical map of the xenopus tropicalis genome
    JOURNAL   Unpublished (2003)
    COMMENT   Contact: Richard K Wilson
              Genome Sequencing Center
              Washington University School of Medicine
              Email: submissions@watson.wustl.edu
              Insert Length: 175000   Std Error: 0.00
              Seq primer: RM1 TACGACTCACTATAGGGAGA
              Class: BAC ends
              High quality sequence start: 11
              High quality sequence stop: 810.
  FEATURES             Location/Qualifiers
       source          1..885
                       /organism="Xenopus tropicalis"
                       /mol_type="genomic DNA"
                       /strain="Nigerian frog"
                       /db_xref="taxon:8364"
                       /clone="CH216-138F20"
                       /sex="male"
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```
                                         LOCUS           CK287297              856 bp    mRNA    linear   EST 02-AUG-2004
                                         DEFINITION      EST75019 Nicotiana benthamiana mixed tissue cDNA library,
                                                         normalized, full-length Nicotiana benthamiana cDNA clone NBMB815 5'
                                                         end, mRNA sequence.
                                         ACCESSION       CK287297
                                         VERSION         CK287297.1  GI:39863696
                                         KEYWORDS        EST.
                                         SOURCE          Nicotiana benthamiana
                                         ORGANISM        Nicotiana benthamiana
                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                         Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
                                                         asterids; lamiids; Solanales; Solanaceae; Nicotiana.
                                         REFERENCE       1  (bases 1 to 856)
                                         AUTHORS         Buell,C.R., Hart,A., Zismann,V., Karamycheva,S.A., Day,B.,
                                                         Staskawicz,B., Jin,H. and Baker,B.
                                         TITLE           Generation of EST sequences from Nicotiana benthamiana
                                         JOURNAL         Unpublished (2003)
                                         COMMENT         Other_ESTs: EST750020
                                                         Contact: Robin Buell
                                                         The Institute for Genomic Research
                                                         9712 Medical Center Dr, Rockville, MD 20850, USA
                                                         Email: potato-array@tigr.org
                                                         Clones can be requested from the University of Arizona Genomics
                                                         Institute via http://genome.arizona.edu/orders/ .
                                                         Seq primer: ATT TAG GTG ACA CTA TAG.
                                         FEATURES        Location/Qualifiers
                                         source          1..856
                                                         /organism="Nicotiana benthamiana"
                                                         /mol_type="mRNA"
                                                         /db_xref="taxon:4100"
                                                         /clone="NBMB815"
                                                         /tissue_type="abiotic and biotic stress-treated leaves,
                                                         callus tissue and root tissue"
                                                         /clone_lib="Nicotiana benthamiana mixed tissue cDNA
                                                         library, normalized, full-length"
                                                         /note="Vector: pCMVSport6.1; Site 1: EcoRI; Site_2: NotI;
                                                         supplier: RNA was isolated from Nicotiana benthamiana
                                                         tissues that include callus, roots from liquid culture
                                                         grown plants, heat-stressed leaves (38 C, 3 hr and 6 hr),
                                                         cold-stressed leaves (5 C 3 hr, 6hr), and pathogen
                                                         challenged leaves (Pseudomonas syringae pv tomato 12 hr;
                                                         Xanthomonas campestris pv campestris 12 hr, 18hr;
                                                         Pseudomonas syringae pv phaseolicola 18hr, and Xanthomonas
                                                         campestris pv vesicatoria 18hr). RNA was isolated from
                                                         these tissues and pooled in approximately equal molar
                                                         amounts."

ORIGIN                                   ORIGIN

Query Match      16.3%;  Score 859.2; DB 9; Length 885;    Query Match      16.0%;  Score 843; DB 7; Length 856;
Best Local Similarity  99.4%;  Pred. No. 1e-235;            Best Local Similarity  100.0%;  Pred. No. 4.7e-231;
Matches 872; Conservative   0;  Mismatches   4; Indels  1; Gaps  1;   Matches 843; Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;
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Qy   4389  TCGCCGTCGGCATGCGCGCCTTGAGCCTGGCGGAACAGTTCGGCTGCGGCGAGCCCCTGA  4448
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    556  TCGCCGTGGGCATGCGCGCCTTGAGCCTGGCGGAACAGTTCGGCTGCGGCGAGCCCCTGA   497

Qy   4449  TGCTCTTCGTCCAGATCATCCTGATCGACAACAGACCGGCTTCCATCCGAGTACGTGCTCGC  4508
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    496  TGCTCTTCGTCCAGATCATCCTGATCGACAACAGACCGGCTTCCATCCGAGTACGTGCTCGC   437

Qy   4509  TCGATGCGATGTTTCGCTTGGTGGTCGAATGGGCAGGTAGCCGGATCAAGCGTATGCAGC  4568
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    436  TCGATGCGATGTTTCGCTTGGTGGTCGAATGGGCAGGTAGCCGGATCAAGCGTATGCAGC   377

Qy   4569  CGCCGCATTGCATCAGCCATGATGATACTTTCTCGGCAGGAGCAAGGTGAGATGACAGG  4628
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    376  CGCCGCATTGCATCAGCCATGATGATACTTTCTCGGCAGGAGCAAGGTGAGATGACAGG   317

Qy   4629  AGATCCTGCCCCGGCACTTCGCCCAATAGCAGCCAGTCCCTTCCCGCTTCAGTGACAACG  4688
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    316  AGATCCTGCCCCGGCACTTCGCCCAATAGCAGCCAGTCCCTTCCCGCTTCAGTGACAACG   257

Qy   4689  TCGAGCACAGCTGCGCAAGGAACGCCCGTCGTGGCCACGATAGCCGCGCCTGCCTCG  4748
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    256  TCGAGCACAGCTGCGCAAGGAACGCCCGTCGTGGCCAGCACGATAGCCGCGCCTGCCTCG   197

Qy   4749  TCCTGCAGTTCATTCAGGGCACCCGGACAGGTCGGTCTTGACAAAAAGAACCGGGGCCCC  4808
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    196  TCCTGCAGTTCATTCAGGGCACCCGGACCACCGGTCGGTCTTGACAAAAAGAACCGGGGCCCC   137

Qy   4809  TGCGCTGACACAGCCGGAACACCGGCGGCATCAGAGCAGCCGATTGTCGTTGTGTGCCCAGTCA  4868
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    136  TGCGCTGACACAGCCGGAACACGGCGGCATCAGAGCAGCCGATTGTCGTTGTGTGCCCAGTCA    77

Qy   4869  TAGCCGAATAGCCTCTCCACCCAAGCGGCCGGAGAACCTGCCTGCAATCCATCTTGTTCA  4928
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     76  TAGCCGAATAGCCTCTCCACCCAAGCGGCCGGAGAACCTGCCTGCAATCCATCTTGTTCA    17

Qy   4929  ATC  4931
            |||
Db     16  ATC  14
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RESULT 15
CL021193
LOCUS   CL021193   CH216-8A16_RM1.1 CH216 Xenopus tropicalis genomic clone CH216-8A16,   1025 bp   DNA   linear   GSS   31-DEC-2003
DEFINITION CH216-8A16_RM1.1 CH216 Xenopus tropicalis genomic clone CH216-8A16, genomic survey sequence.
ACCESSION   CL021193
VERSION   CL021193.1 GI:40463006
KEYWORDS   GSS.
SOURCE   Xenopus tropicalis (western clawed frog)
  ORGANISM Xenopus tropicalis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
            Xenopodinae; Xenopus; Silurana.
REFERENCE   1 (bases 1 to 1025)
  AUTHORS   Kremitzki,C., Carter,J., McPherson,J., Warren,W., Graves,T.,
            Mardis,E. and Wilson,R.
  TITLE   A physical map of the xenopus tropicalis genome
  JOURNAL   Unpublished (2003)
COMMENT   Contact: Richard K Wilson
            Washington University School of Medicine
            Genome Sequencing Center
            Email: submissions@watson.wustl.edu
            Insert Length: 175000   Std Error: 0.00
            Seq primer: RM1 TACGACTCACTATAGGGAGA
            Class: BAC ends
            High quality sequence start: 72
            High quality sequence stop: 837.
FEATURES   Location/Qualifiers
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                     /organism="Xenopus tropicalis"
                     /mol_type="genomic DNA"
                     /strain="Nigerian frog"
                     /db_xref="taxon:8364"
                     /clone="CH216-8A16"
                     /sex="male"
                     /cell_line="Stock 248 F7A2, inbred N7"
                     /clone_lib="CH216"
                     /note="Vector: pTARBAC2.1; CHORI-216 Xenopus tropicalis
                     BAC library"
ORIGIN

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Query Match        15.5%;   Score 820.6; DB 9;   Length 1025;
Best Local Similarity 95.6%;   Pred. No. 1.5e-224;
Matches 898;   Conservative 0;  Mismatches 34;   Indels 7;   Gaps 5;
```

```
Qy   2701  GCTGTCTCAGACGTAATCATGGTCATAG-CTGTTTCCTGTGTGAAATTGTTATC--CGCTCA  2758
               || ||| |||||||||||||||| ||||   ||||||||||||||| ||| ||||||||||
Db     88  GCAATCTTGGCGTAATCATGGTCATAGTCTGTTTCCTGTGTGAAATTGTTATCTCGCTCA   147

Qy   2759  CAATTCCACACACATACAGAGCCGGAAGCAGCATAAAGTGTAAAGCTGGGGTGCCTAATGAG  2818
               ||||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||
Db    148  CAATTCCACACAACTTACTACCCGGAACGATAAAATGTAAAGCCGGGGTGCCTAATGAG   207

Qy   2819  TGAGCTAACTCACATTAATTGCGTGCGCTCACTGCCC--GCTTTCCAGTCGGGAAACCT  2876
               ||| |||||||||||||||||| |||||| |||||||  |||||| |||||||||||||||
Db    208  TGACCTAACTCACATTAATTGCGTGCGCTCACTGCCCAGACTTTCCAATCGGGAAACCT   267

Qy   2877  GTCGTGCCAGCTGCATTAATGAATCGGCCAAGCGCGCGG--GAGAGGCGGTTTGCGTATT  2934
               |||||||||||||||||| ||||| ||||||||||||||   ||||||||||||||||||
Db    268  GTCGTGCCAGCTGCATTAATGAATCGGCCAACACGGGGGAGAGGCGGTTTGCGTATT   327

Qy   2935  GGGCGCTCTCCGCTTCCGCTTCCTCCTGCCATTGTCGTTGTTGCGGCGGCA  2994
               ||||||||||||||||||||||||| ||||||||||| |||||||||||||||
Db    328  GGGCGCTCTCCGCTTCCGCTTCCTCCTGCGCTGACTGCGTTCGGCGTGCAGCGA   387

Qy   2995  GCGGTATCAGCTCACTCAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCA  3054
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    388  GCGGTATCAGCTCACTCAAAGGCGGTAATACAGTTATCCACAAAATCATGGGGATAACGCA   447

Qy   3055  GAAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTG  3114
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    448  GAAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTA   507

Qy   3115  CTGGCGGTTTTTCCATAGGCTCCGCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAGT  3174
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    508  CTGGCGGTTTTTCCATAAGCTCCGCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAGT   567

Qy   3175  CAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCC  3234
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    568  CAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCC   627

Qy   3235  CTCGTGCGCTCTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGATACCTTTCTCCCT  3294
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    628  CTCGTGCGCTCTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCT   687

Qy   3295  TCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCCAGTTCGGTGTAGTC  3354
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    688  TCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGTC   747

Qy   3355  GTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCGTTCAGCCCGACCGCTGCGCCTTA  3414
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    748  GTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCGTTCAGCCCGACCGCTGCGCCTTA   807

Qy   3415  TCCGGTAACTATCGTCTTGAGTCCAACCGGTAAGACGACTTATCGGCCACTGGCAGCA  3474
               ||| || |||| ||| |||||||||||||||||||||||||||||||||||||||
Db    808  TCCGGTAACTATCGTCTTGAGTCCAACCGGTAAGACGACTTATCGGCCACTGGCAGCA   867

Qy   3475  GCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAG  3534
               ||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    868  GCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAG   927

Qy   3535  TGGTGGCTAACTACGGCTACTAGAAGAACAGTATTTGGTATCGCGCTCTGCTGAAG  3594
               ||||||||||||||| ||||| |||| |||||  |||||||| ||||||||||||
Db    928  TGTTGGCCTAACTACGGCTAC-CTAGAAAAAACCACTATTTGGTATCTGCGCTCTGCGCGGTAA   986
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Qy    3595 CCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCC 3633
           ||||||||||||||||||||| | ||||||||||||||||
Db     987 CCAGTTACCTTCGGAAAAAAATTGGGTAGCTCTTGATCC 1025
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Search completed: July 3, 2005, 18:58:01
Job time : 1542 secs